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UTILITY PATENT APPLICATION TRANSMITTAL

(Only for new nonprovisional applications under 37 C.F.R. § 1.53(b))

Attorney Docket No.	MBI-0010
First Inventor or Application Identifier	Heard
Title	Disease-Induced Polynucleotides
Express Mail Label No.	EK483897023US

APPLICATION ELEMENTS

See MPEP chapter 600 concerning utility patent application contents.

ADDRESS TO: Assistant Commissioner for Patents, Box Patent Application, Washington, DC 20231

1. [X] * Fee Transmittal Form (e.g., PTO/SB/17) (Submit an original and a duplicate for fee processing)
2. [X] Specification [Total Pages 29] (preferred arrangement set forth below)
   - Descriptive title of the Invention
   - Cross References to Related Applications
   - Statement Regarding Fed sponsored R & D
   - Reference to Microfiche Appendix
   - Background of the Invention
   - Brief Summary of the Invention
   - Brief Description of the Drawings (if filed)
   - Detailed Description
   - Claim(s)
   - Abstract of the Disclosure
3. [X] Drawing(s) (35 U.S.C. 113) [Total Sheets 4]
4. Oath or Declaration [Total Pages]
   a. [X] Newly executed (original or copy)
   b. [ ] Copy from a prior application (37 C.F.R. § 1.63(d)) (for continuation/divisional with Box 16 completed)
      i. [ ] DELETION OF INVENTOR(S) Signed statement attached deleting inventor(s) named in the prior application, see 37 C.F.R. §§ 1.63(d)(2) and 1.33(b).

NOTE FOR ITEMS 1 & 13: IN ORDER TO BE ENTITLED TO PAY SMALL ENTITY FEES, A SMALL ENTITY STATEMENT IS REQUIRED (37 C.F.R. § 1.27), EXCEPT IF ONE FILED IN A PRIOR APPLICATION IS RELIED UPON (37 C.F.R. § 1.28).

5. [ ] Microfiche Computer Program (Appendix)
6. Nucleotide and/or Amino Acid Sequence Submission (if applicable, all necessary)
   a. [X] Computer Readable Copy
   b. [X] Paper Copy (identical to computer copy)
   c. [X] Statement verifying identity of above copies

ACCOMPANYING APPLICATION PARTS

7. [X] Assignment Papers (cover sheet & document(s))
8. [X] 37 C.F.R.§3.73(b) Statement (when there is an assignee) [ ] Power of Attorney
9. [ ] English Translation Document (if applicable)
10. [ ] Information Disclosure Statement (IDS)/PTO-1449 [ ] Copies of IDS Citations
11. [ ] Preliminary Amendment
12. [ ] Return Receipt Postcard (MPEP 503) (Should be specifically itemized)
13. [X] * Small Entity Statement(s) (PTO/SB/09-12) [ ] Statement filed in prior application, Status still proper and desired
14. [ ] Certified Copy of Priority Document(s) (if foreign priority is claimed)
15. [ ] Other: ....

16. If a CONTINUING APPLICATION, check appropriate box, and supply the requisite information below and in a preliminary amendment:

[ ] Continuation [ ] Divisional [ ] Continuation-in-part (CIP) of prior application No: ______/______

Prior application information: Examiner ______ Group / Art Unit: ______

For CONTINUATION or DIVISIONAL APPS only: The entire disclosure of the prior application, from which an oath or declaration is supplied under Box 4b, is considered a part of the disclosure of the accompanying continuation or divisional application and is hereby incorporated by reference. The incorporation can only be relied upon when a portion has been inadvertently omitted from the submitted application parts.

17. CORRESPONDENCE ADDRESS

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Signature	Karen Guerrero	Date	3/22/00

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application

Inventor(s): Jacqueline Heard et al.

Application No.: Unassigned

Filed: Herewith

Title: Disease-induced polynucleotides

VERIFIED STATEMENT CLAIMING SMALL ENTITY STATUS
37 C.F.R. § 1.9(d) AND 1.27(c) - SMALL BUSINESS CONCERN

I hereby declare that I am an official of the small business concern empowered to act on behalf of the concern identified below.

Name: Mendel Biotechnology, Inc.

Address: 21375 Cabot Boulevard, Hayward, California 94545

I hereby declare that the above identified small business concern qualifies as a small business concern as defined in 13 C.F.R. § 121.12, and reproduced in 37 C.F.R. § 1.9(d), for purposes of paying reduced fees under Section 41(a) and (b) of Title 35 U.S.C. in that the number of employees of the concern, including those of its affiliates, does not exceed 500 persons. For purposes of this statement, (1) the number of employees of the business concern is the average over the previous fiscal year of the concern of the persons employed on a full-time, part-time or temporary basis during each of the pay periods of the fiscal year, and (2) concerns are affiliates of each other when either, directly or indirectly, one concern controls or has the power to control the other, or a third-party or parties controls or has the power to control both.

I hereby declare that rights under contract or law have been conveyed to and remain with the small business concern identified above with regard to the invention.

entitled: Disease-induced polynucleotides

described in the Specification filed herewith

If the rights held by the above-identified small business concern are not exclusive, each individual, concern or organization having rights to the invention is listed below and no rights to the invention are held by any person, other than the inventor, who could not qualify as a small business concern under 37 C.F.R. § 1.9(d) or by any concern which would not qualify as a small business concern under 37 C.F.R. § 1.9(d) or a nonprofit organization under 37 C.F.R. § 1.9(e).

[ ] Individual [X] Small Business Concem [] Nonprofit Organization

I acknowledge the duty to file, in this application or patent, notification of any change in status resulting in loss of entitlement to small entity status prior to paying, or at the time of paying, the earliest of the issue fee or any maintenance fee due after the date on which status as a small business entity is no longer appropriate. (37 C.F.R. § 1.28(b)).

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application, any patent issuing thereon, or any patent to which this verified statement is directed.

Name of Person Signing: Guo-Liang Yu

Title of Person Signing: Senior Vice-President, Research and Development

Address of Person Signing: 21375 Cabot Boulevard, Hayward, California 94545

Signature:

Date: 03/20/2000

DISEASE-INDUCED POLYNUCLEOTIDES

The present invention claims priority in part from US Provisional Application Serial No. 60/125,814 filed March 23, 1999.

FIELD OF THE INVENTION

This invention is in the field of plant molecular biology and relates to compositions and methods for modifying a plant's traits, in particular plant disease tolerance or resistance.

BACKGROUND OF THE INVENTION

Gene expression levels are controlled in part at the level of transcription, and transcription is affected by transcription factors. Transcription factors regulate gene expression throughout the life cycle of an organism and so are responsible for differential levels of gene expression at various developmental stages, in different tissue and cell types, and in response to different stimuli. Transcription factors may interact with other proteins or with specific sites on a target gene sequence to activate, suppress or otherwise regulate transcription. In addition, the transcription of the transcription factors themselves may be regulated.

Because transcription factors are key controlling elements for biological pathways, altering the expression levels of one or more transcription factors may change entire biological pathways in an organism. For example, manipulation of the levels of selected transcription factors may result in increased expression of economically useful proteins or metabolic chemicals in plants or to improve other agriculturally relevant characteristics. Conversely, blocked or reduced expression of a transcription factor may reduce biosynthesis of unwanted compounds or remove an undesirable trait. Therefore, manipulating transcription factor levels in a plant offers tremendous potential in agricultural biotechnology for modifying a plant's traits.

The present invention provides transcription factors for use in modifying a plant's disease tolerance or resistance.

SUMMARY OF THE INVENTION

In one aspect, the present invention relates to a transgenic plant comprising a recombinant polynucleotide. The recombinant polynucleotide comprises a nucleotide sequence encoding a polypeptide comprising at least 6 consecutive amino acids of a sequence selected from the group consisting of protein SEQ ID Nos. 2N, where N=1-56. And the presence of the recombinant polynucleotide alters the disease tolerance or resistance

of the transgenic plant when compared with the same trait of another plant lacking the recombinant polynucleotide.

In one embodiment, the nucleotide sequence encodes a polypeptide comprising a conserved domain which may be 1) a localization domain, 2) an activation domain, 3) a repression domain, 4) an oligomerization domain or 5) a DNA binding domain. In a further embodiment, the nucleotide sequence further comprises a promoter operably linked to the nucleotide sequence. The promoter may be a constitutive or inducible or tissue-active.

In a second aspect, the present invention relates to a method for altering a plant's deisease tolerance or resistance. The method comprises (a) transforming a plant with a recombinant polynucleotide comprising a nucleotide sequence encoding a polypeptide comprising at least 6 consecutive amino acids of a sequence selected from the group consisting of protein SEQ ID Nos. 2N, where N=1-56; (b) selecting transformed plants; and (c) identifying a transformed plant with roots having an altered trait.

In one embodiment, the nucleotide sequence encodes a polypeptide comprising a conserved domain which may be 1) a localization domain, 2) an activation domain, 3) a repression domain, 4) an oligomerization domain or 5) a DNA binding domain. In a further embodiment, the nucleotide sequence further comprises a promoter operably linked to the nucleotide sequence. The promoter may be a constitutive or inducible or tissue-active.

In a third aspect, the present invention relates to a method for altering the expression levels of at least one gene in a plant. The method comprises (a) transforming the plant with a recombinant polynucleotide comprising a nucleotide sequence encoding a polypeptide comprising at least 6 consecutive amino acids of a sequence selected from the group consisting of protein SEQ ID Nos. 2N, where N=1-56; and (b) selecting said transformed plant.

In one embodiment, the nucleotide sequence encodes a polypeptide comprising a conserved domain which may be 1) a localization domain, 2) an activation domain, 3) a repression domain, 4) an oligomerization domain or 5) a DNA binding domain. In a further embodiment, the nucleotide sequence further comprises a promoter operably linked to the nucleotide sequence. The promoter may be a constitutive or inducible or tissue-active.

In a fourth aspect, the present invention relates to another method for altering the disease tolerance of a plant. The method comprises (a) transforming the plant with a recombinant polynucleotide comprising a nucleotide sequence comprising at least 18 consecutive nucleotides of a sequence selected from the group consisting of SEQ ID Nos. 2N-1, where N= 1-56, and SEQ ID Nos. 113-121; and (b) selecting said transformed plant.

In yet another aspect, the present invention is yet another method for altering a plant's trait. The method comprises (a) providing a database sequence; (b) comparing the database sequence with a polypeptide selected from SEQ ID Nos. 2N, where N= 1-56; (c) selecting a database sequence that meets selected sequence criteria; and (d) transforming

said database sequence in the plant. Alternatively, the database sequence can be compared with a polynucleotide selected from SEQ ID Nos. 2N-1, where N= 1-56 or SEQ ID Nos. 113-121.

In a further aspect, the present invention is method for altering a plant's trait, and the method entails (a) providing a test polynucleotide; (b) hybridizing the test polynucleotide with a polynucleotide selected from SEQ ID Nos. 2N-1, where N= 1-56 or SEQ ID Nos. 113-121 at low stringency; and (c) transforming the hybridizing test polynucleotide in a plant to alter a trait of the plant.

BRIEF DESCRIPTION OF THE FIGURES

Figures 1a-1e provide a table of exemplary polynucleotide and polypeptide sequences of the invention. The table includes from left to right for each sequence: the SEQ ID No., the internal code reference number, the transcription factor family of the sequence, particular DNA or protein fragments for each sequence, whether the sequence is a polynucleotide or polypeptide sequence, identification of the coding sequence for each full length and identification of any conserved domains for the polypeptide sequences.

DETAILED DESCRIPTION OF THE INVENTION

DEFINITIONS

A "recombinant polynucleotide" is a nucleotide sequence comprising a gene coding sequence or a fragment thereof (comprising at least 18 consecutive nucleotides, preferably at least 30 consecutive nucleotides, and more preferably at least 50 consecutive nucleotides). Additionally, the polynucleotide may comprise a promoter, an intron, an enhancer region, a polyadenylation site, a translation initiation site, 5' or 3' untranslated regions, a reporter gene, a selectable marker or the like. The polynucleotide may comprise single stranded or double stranded DNA or RNA. The polynucleotide may comprise modified bases or a modified backbone. The polynucleotide may be genomic, a transcript (such as an mRNA) or a processed nucleotide sequence (such as a cDNA). The polynucleotide may comprise a sequence in either sense or antisense orientations.

A "recombinant polynucleotide" is a polynucleotide that is not in its native state, e.g., the polynucleotide is comprised of a nucleotide sequence not found in nature or the polynucleotide is separated from nucleotide sequences with which it typically is in proximity or is next to nucleotide sequences with which it typically is not in proximity.

An "recombinant polypeptide" is a polypeptide derived from the translation of a recombinant polynucleotide or is more enriched in a cell than the polypeptide in its natural

state in a wild type cell, e.g. more than 5% enriched, more than 10% enriched or more than 20% enriched and is not the result of a natural response of a wild type plant or is separated from other components with which it is typically associated with in a cell.

A "transgenic plant" may refer to a plant that contains genetic material not normally found in a wild type plant of the same species, or in a naturally occurring variety or in a cultivar, and which has been introduced into the plant by human manipulation. A transgenic plant is a plant that may contain an expression vector or cassette. The expression cassette comprises a gene coding sequence and allows for the expression of the gene coding sequence. The expression cassette may be introduced into a plant by transformation or by breeding after transformation of a parent plant.

A transgenic plant refers to a whole plant as well as to a plant part, such as seed, fruit, leaf, or root, plant tissue, plant cells or any other plant material, and progeny thereof.

The phrase "altered expression" in reference to polynucleotide or polypeptide expression refers to an expression pattern in the transgenic plant that is different from the expression pattern in the wild type plant or a reference; for example, by expression in a cell type other than a cell type in which the sequence is expressed in the wild type plant, or by expression at a time other than at the time the sequence is expressed in the wild type plant, or by a response to different inducible agents, such as hormones or environmental signals, or at different expression levels (either higher or lower) compared with those found in a wild type plant. The term also refers to lowering the levels of expression to below the detection level or completely abolishing expression. The resulting expression pattern may be transient or stable, constitutive or inducible.

A "transcription factor" (TF) refers to a polynucleotide or polypeptide that controls the expression of a gene or genes either directly by binding to one or more nucleotide sequences associated with a gene coding sequence or indirectly by affecting the level or activity of other polypeptides that do bind directly or indirectly to one or more nucleotide sequences associated with a gene coding sequence. A TF, in this definition, includes any polypeptide that can activate or repress transcription of a single gene or a number of genes. This polypeptide group includes, but is not limited to, DNA binding proteins, protein kinases, protein phosphatases, GTP-binding proteins and receptors.

The transcription factor sequence may comprise a whole coding sequence or a fragment or domain of a coding sequence. A "fragment or domain", as referred to polypeptides, may be a portion of a polypeptide which performs at least one biological function of the intact polypeptide in substantially the same manner or to a similar extent as does the intact polypeptide. A fragment may comprise, for example, a DNA binding domain that binds to a specific DNA promoter region, an activation domain or a domain for protein-protein interactions. Fragments may vary in size from as few as 6 amino acids to the length of the

intact polypeptide, but are preferably at least 30 amino acids in length and more preferably at least 60 amino acids in length. In reference to a nucleotide sequence "a fragment" refers to any sequence of at least consecutive 18 nucleotides, preferably at least 30 nucleotides, more preferably at least 50, of any of the sequences provided herein. Exemplary polynucleotides or polypeptides comprise a sequence provided in the Sequence Listing as SEQ ID No.1 (G1043), SEQ ID No.2 (G1043 protein), SEQ ID No.3 (G759), SEQ ID No.4 (G759 protein), SEQ ID No.5 (G185), SEQ ID No.6 (G185 protein), SEQ ID No.7 (G629), SEQ ID No.8 (G629 protein), SEQ ID No.9 (G435), SEQ ID No.10 (G435 protein), SEQ ID No.11 (G4), SEQ ID No.12 (G4 protein), SEQ ID No.13 (G1035), SEQ ID No.14 (G1035 protein), SEQ ID No.15 (G179), SEQ ID No.16 (G179 protein), SEQ ID No.17 (G28), SEQ ID No.18 (G28 protein), SEQ ID No.19 (G1241), SEQ ID No.20 (G1241 protein), SEQ ID No.21 (G19), SEQ ID No.22 (G19 protein), SEQ ID No.23 (G503), SEQ ID No.24 (G503 protein), SEQ ID No.25 (G263), SEQ ID No.26 (G263 protein), SEQ ID No.27 (G921), SEQ ID No.28 (G921 protein), SEQ ID No.29 (G1275), SEQ ID No.30 (G1275 protein), SEQ ID No.31 (G242), SEQ ID No.32 (G242 protein), SEQ ID No.33 (G1006), SEQ ID No.34 (G1006 protein), SEQ ID No.35 (G1049), SEQ ID No.36 (G1049 protein), SEQ ID No.37 (G502), SEQ ID No.38 (G502 protein), SEQ ID No.39 (G239), SEQ ID No.40 (G239 protein), SEQ ID No.41 (G555), SEQ ID No.42 (G555 protein), SEQ ID No.43 (G352), SEQ ID No.44 (G352 protein), SEQ ID No.45 (G1352), SEQ ID No.46 (G1352 protein), SEQ ID No.47 (G1089), SEQ ID No.48 (G1089 protein), SEQ ID No.49 (G553), SEQ ID No.50 (G553 protein), SEQ ID No.51 (G1221), SEQ ID No.52 (G1221 protein), SEQ ID No.53 (G580), SEQ ID No.54 (G580 protein), SEQ ID No.55 (G270), SEQ ID No.56 (G270 protein), SEQ ID No.57 (G201), SEQ ID No.58 (G201 protein), SEQ ID No.59 (G1417), SEQ ID No.60 (G1417 protein), SEQ ID No.61 (G233), SEQ ID No.62 (G233 protein), SEQ ID No.63 (G920), SEQ ID No.64 (G920 protein), SEQ ID No.65 (G867), SEQ ID No.66 (G867 protein), SEQ ID No.67 (G659), SEQ ID No.68 (G659 protein), SEQ ID No.69 (G620), SEQ ID No.70 (G620 protein), SEQ ID No.71 (G596), SEQ ID No.72 (G596 protein), SEQ ID No.73 (G511), SEQ ID No.74 (G511 protein), SEQ ID No.75 (G471), SEQ ID No.76 (G471 protein), SEQ ID No.77 (G385), SEQ ID No.78 (G385 protein), SEQ ID No.79 (G261), SEQ ID No.80 (G261 protein), SEQ ID No.81 (G25), SEQ ID No.82 (G25 protein), SEQ ID No.83 (G610), SEQ ID No.84 (G610 protein), SEQ ID No.85 (G229), SEQ ID No.86 (G229 protein), SEQ ID No.87 (G221), SEQ ID No.88 (G221 protein), SEQ ID No.89 (G186), SEQ ID No.90 (G186 protein), SEQ ID No.91 (G562), SEQ ID No.92 (G562 protein), SEQ ID No.93 (G255), SEQ ID No.94 (G255 protein), SEQ ID No.95 (G3), SEQ ID No.96 (G3 protein), SEQ ID No.97 (G713), SEQ ID No.98 (G713 protein), SEQ ID No.99 (G515), SEQ ID No.100 (G515 protein), SEQ ID No.101 (G390), SEQ ID No.102 (G390 protein), SEQ ID No.103 (G1034), SEQ ID No.104 (G1034 protein), SEQ ID No.105 (G1149), SEQ ID No.106 (G1149 protein), SEQ ID No.107 (G1334), SEQ ID No.108 (G1334 protein), SEQ ID No.109 (G1650), SEQ ID

No.110 (G1650 protein), SEQ ID No.111 (G241), SEQ ID No.112 (G241 protein), SEQ ID No.113 (G348), SEQ ID No.114 (G171), SEQ ID No.115 (G521), SEQ ID No.116 (G1274), SEQ ID No.117 (G182), SEQ ID No.118 (G1290), SEQ ID No.119 (G374), SEQ ID No.120 (G682) and SEQ ID No.121 (G501).

A "conserved domain" refers to a polynucleotide or polypeptide fragment that is more conserved at a sequence level than other fragments when the polynucleotide or polypeptide is compared with homologous genes or proteins from other plants. The conserved domain may be 1) a localization domain, 2) an activation domain, 3) a repression domain, 4) an oligomerization domain or 5) a DNA binding domain.

A nucleotide sequence is "operably linked" when it is placed into a functional relationship with another nucleotide sequence. For example, a promoter or enhancer is operably linked to a gene coding sequence if the presence of the promoter or enhancer increases the level of expression of the gene coding sequence.

"Trait" refers to a physiological, morphological, biochemical or physical characteristic of a plant or particular plant material or cell. This characteristic may be visible to the human eye, such as seed or plant size, or be measured by biochemical techniques, such as the protein, starch or oil content of seed or leaves or by the observation of the expression level of genes by employing Northerns, RT PCR, microarray gene expression assays or reporter gene expression systems or be measured by agricultural observations such as stress tolerance, yield or disease resistance.

"Trait modification" refers to a detectable difference in a characteristic in a transgenic plant expressing a polynucleotide or polypeptide of the present invention relative to a plant not doing so, such as a wild type plant. The trait modification may entail at least a 5% increase or decrease in an observed trait (difference), at least a 10% difference, at least a 20% difference, at least a 30%, at least a 50%, at least a 70%, at least a 100% or a greater difference. It is known that there may be a natural variation in the modified trait. Therefore, the trait modification observed entails a change in the normal distribution of the trait in transgenic plants compared with the distribution observed in wild type plant.

Trait modifications of particular interest include those to seed (embryo), fruit, root, flower, leaf, stem, shoot, seedling or the like, including: enhanced tolerance to environmental conditions including freezing, chilling, heat, drought, water saturation, radiation and ozone; enhanced resistance to microbial, fungal or viral diseases; resistance to nematodes, decreased herbicide sensitivity, enhanced tolerance of heavy metals (or enhanced ability to take up heavy metals), enhanced growth under poor photoconditions (e.g., low light and/or short day length), or changes in expression levels of genes of interest. Other phenotypes that may be modified relate to the production of plant metabolites, such as variations in the production of taxol, tocopherol, tocotrienol, sterols, phytosterols, vitamins, wax monomers,

anti-oxidants, amino acids, lignins, cellulose, tannins, prenyllipids (such as chlorophylls and carotenoids), glucosinolates, and terpenoids, enhanced or compositionally altered protein or oil production (especially in seeds), or modified sugar (insoluble or soluble) and/or starch composition. Physical plant characteristics that may be modified include cell development (such as the number of trichomes), fruit and seed size and number, yields of plant parts such as stems, leaves and roots, the stability of the seeds during storage, characteristics of the seed pod (e.g., susceptibility to shattering), root hair length and quantity, internode distances, or the quality of seed coat. Plant growth characteristics that may be modified include growth rate, germination rate of seeds, vigor of plants and seedlings, leaf and flower senescence, male sterility, apomixis, flowering time, flower abscission, rate of nitrogen uptake, biomass or transpiration characteristics, as well as plant architecture characteristics such as apical dominance, branching patterns, number of organs, organ identity, organ shape or size.

Of particular interest are traits relating to increased disease resistance or tolerance of a plant, such as alterations in cell wall composition, trichome number or structure, callose induction, phytoalexin induction, alterations in the cell death response or the like. These transgenic plants may be more resistant to biotrophic or necrotrophic pathogens such as a fungus, bacterium, mollicute, virus, nematode, a parasitic higher plant or the like and associated diseases. Another desirable phenotype is a change in the overall gene expression pattern of the plant in response to disease.

1. The Sequences

We have discovered particular plant transcription factors (TFs) that are induced when plants are exposed to either biotropic or necrotropic pathogens.. These transgenic plants may be more resistant to biotrophic or necrotrophic pathogens such as a fungus, bacterium, mollicute, virus, nematode, a parasitic higher plant or the like and associated diseases, in particular, pathogens such as *Fusarium oxysporum*, *Erysyphe orontii* and other powdery mildews, *Sclerotinia spp.*, soil-borne oomycetes, foliar oomycetes, *Botrytis spp.*, *Rhizoctonia spp*, *Verticillium dahliae/albo-atrum*, *Alternaria spp.*, rusts, *Mycosphaerella spp*, *Fusarium solani*, or the like. The diseases include fungal diseases such as rusts, smuts, wilts, yellows, root rot, leaf drop, ergot, leaf blight of potato, brown spot of rice, leaf blight, late blight, powdery mildew, downy mildew, and the like; viral diseases such as sugarcane mosaic, cassava mosaic, sugar beet yellows, plum pox, barley yellow dwarf, tomato yellow leaf curl, tomato spotted wilt virus, and the like; bacterial diseases such as citrus canker, bacterial leaf blight, bacterial will, soft rot of vegetables, and the like; nematode diseases such as root knot, sugar beet cyst nematode or the like.

These transcription factors can be used to modulate a plant's response to disease. The plant transcription factors may belong to one of the following transcription factor families:

the AP2 (APETALA2) domain transcription factor family (Riechmann and Meyerowitz (1998) *J. Biol. Chem.* 379:633-646); the MYB transcription factor family (Martin and Paz-Ares, (1997) *Trends Genet.* 13:67-73); the MADS domain transcription factor family (Riechmann and Meyerowitz (1997) *J. Biol. Chem.* 378:1079-1101); the WRKY protein family (Ishiguro and Nakamura (1994) *Mol. Gen. Genet.* 244:563-571); the ankyrin-repeat protein family (Zhang et al. (1992) *Plant Cell* 4:1575-1588); the zinc finger protein (Z) family (Klug and Schwabe (1995) *FASEB J. 9:* 597-604); the homeobox (HB) protein family (Duboule (1994) *Guidebook to the Homeobox Genes,* Oxford University Press); the CAAT-element binding proteins (Forsburg and Guarente (1989) *Genes Dev.* 3:1166-1178); the squamosa promoter binding proteins (SPB) (Klein et al. (1996) *Mol. Gen. Genet.* 1996 250:7-16); the NAM protein family (Souer et al. (1996) Cell 85:159-170); the IAA/AUX proteins (Rouse et al. (1998) *Science* 279:1371–1373); the HLH/MYC protein family (Littlewood et al. (1994) *Prot. Profile* 1:639-709); the DNA-binding protein (DBP) family (Tucker et al. (1994) *EMBO J.* 13:2994-3002); the bZIP family of transcription factors (Foster et al. (1994) *FASEB J.* 8:192-200); the Box P-binding protein (the BPF-1) family (da Costa e Silva et al. (1993) *Plant J.* 4:125-135); the high mobility group (HMG) family (Bustin and Reeves (1996) *Prog. Nucl. Acids Res. Mol. Biol.* 54:35-100); the scarecrow (SCR) family (Di Laurenzio et al. (1996) *Cell* 86:423-433); the GF14 family (Wu et al. (1997) *Plant Physiol.* 114:1421-1431); the polycomb (PCOMB) family (Kennison (1995) *Annu. Rev. Genet.* 29:289-303); the teosinte branched (TEO) family (Luo et al. (1996) *Nature* 383:794-799; the ABI3 family (Giraudat et al. (1992) *Plant Cell* 4:1251-1261); the triple helix (TH) family (Dehesh et al. (1990) *Science* 250:1397-1399); the EIL family (Chao et al. (1997) *Cell* 89:1133-44); the AT-HOOK family (Reeves and Nissen (1990) *Journal of Biological Chemistry* 265:8573-8582); the S1FA family (Zhou et al. (1995) *Nucleic Acids Res.* 23:1165-1169); the bZIPT2 family (Lu and Ferl (1995) *Plant Physiol.* 109:723); the YABBY family (Bowman et al. (1999) *Development* 126:2387-96); the PAZ family (Bohmert et al. (1998) *EMBO J.* 17:170-80); a family of miscellaneous (MISC) transcription factors including the DPBF family (Kim et al. (1997) *Plant J.* 11:1237-1251) and the SPF1 family (Ishiguro and Nakamura (1994) *Mol. Gen. Genet.* 244:563-571); the golden (GLD) family (Hall et al. (1998) *Plant Cell* 10:925-936).

Producing transgenic plants with modified expression levels of one or more of these transcription factors compared with those levels found in a wild type or reference plant may be used to modify a plant's traits. The effect of modifying the expression levels of a particular transcription factor on the traits of a transgenic plant is described further in the Examples.

The polynucleotides and polypeptides are provided in the Sequence Listing and are tabulated in Figure 1. Figure 1 identifies a SEQ ID No., its corresponding GID number, the transcription factor family to which the sequence belongs, fragments derived from the sequences, whether the sequence is a polynucleotide or a polypeptide sequence, the full

length coding sequences and conserved domains. We have also identified domains or fragments derived from the sequences. The numbers indicating the fragment location for the DNA sequences may be from either 5' or 3' end of the DNA. For the protein sequences the fragment location is determined from the N-terminus of the protein and may include adjacent amino acid sequences, such as for example for SEQ ID No. 2 an additional 10, 20, 40, 60 or 100 amino acids in either N-terminal or C-terminal direction of the described fragments.

The identified polypeptide fragments may be linked to fragments or sequences derived from other transcription factors so as to generate additional novel sequences, such as by employing the methods described in Short, PCT publication WO9827230, entitled "Methods and Compositions for Polypeptide Engineering" or in Patten et al., PCT publication WO9923236, entitled "Method of DNA Shuffling". Alternatively, the identified fragment may be linked to a transcription activation domain. A transcription activation domain assists in initiating transcription from a DNA binding site. A common feature of some activation domains is that they are designed to form amphiphilic alpha helices with excess positive or negative charge (Giniger and Ptashne (1987) Nature 330:670-672, Gill and Ptashne (1987) Cell 51:121-126, Estruch et al (1994) Nucl. Acids Res. 22:3983-3989). Examples include the transcription activation region of VP16 or GAL4 (Moore et al. (1998) Proc. Natl. Acad. Sci. USA 95: 376-381; and Aoyama et al. (1995) Plant Cell 7:1773-1785), peptides derived from bacterial sequences (Ma and Ptashne (1987) Cell 51; 113-119) and synthetic peptides (Giniger and Ptashne, supra).

The isolated polynucleotides and polypeptides may be used to modify plant development, physiology or biochemistry such that the modified plants have a trait advantage over wild type plants. The identified polynucleotide fragments are also useful as nucleic acid probes and primers. A nucleic acid probe is useful in hybridization protocols, including protocols for microarray experiments. Primers may be annealed to a complementary target DNA strand by nucleic acid hybridization to form a hybrid between the primer and the target DNA strand, and then extended along the target DNA strand by a DNA polymerase enzyme. Primer pairs can be used for amplification of a nucleic acid sequence, e.g., by the polymerase chain reaction (PCR) or other nucleic-acid amplification methods. See Sambrook et al., *Molecular Cloning. A Laboratory Manual*, Ed. 2, Cold Spring Harbor Laboratory Press, New York (1989) and Ausubel et al. (eds) *Current Protocols in Molecular Biology*, John Wiley & Sons (1998).

2. Identification of Homologous Sequences (Homologs)

Homologous sequences to those provided in the Sequence Listing derived from *Arabidopsis thaliana* or from other plants may be used to modify a plant trait. Homologous sequences may be derived from any plant including monocots and dicots and in particular

agriculturally important plant species, including but not limited to, crops such as soybean, wheat, corn, potato, cotton, rice, oilseed rape (including canola), sunflower, alfalfa, sugarcane and turf; or fruits and vegetables, such as banana, blackberry, blueberry, strawberry, and raspberry, cantaloupe, carrot, cauliflower, coffee, cucumber, eggplant, grapes, honeydew, lettuce, mango, melon, onion, papaya, peas, peppers, pineapple, spinach, squash, sweet corn, tobacco, tomato, watermelon, rosaceous fruits (such as apple, peach, pear, cherry and plum) and vegetable brassicas (such as broccoli, cabbage, cauliflower, brussel sprouts and kohlrabi). Other crops, fruits and vegetables whose phenotype may be changed include barley, currant, avocado, citrus fruits such as oranges, lemons, grapefruit and tangerines, artichoke, cherries, nuts such as the walnut and peanut, endive, leek, roots, such as arrowroot, beet, cassava, turnip, radish, yam, sweet potato and beans. The homologs may also be derived from woody species, such pine, poplar and eucalyptus.

Substitutions, deletions and insertions introduced into the sequences provided in the Sequence Listing are also envisioned by the invention. Such sequence modifications can be engineered into a sequence by site-directed mutagenesis (Wu (ed.) *Meth. Enzymol.* (1993) vol. 217, Academic Press). Amino acid substitutions are typically of single residues; insertions usually will be on the order of about from 1 to 10 amino acid residues; and deletions will range about from 1 to 30 residues. In preferred embodiments, deletions or insertions are made in adjacent pairs, e.g., a deletion of two residues or insertion of two residues. Substitutions, deletions, insertions or any combination thereof may be combined to arrive at a sequence. The mutations that are made in the polynucleotide encoding the transcription factor should not place the sequence out of reading frame and should not create complementary regions that could produce secondary mRNA structure.

Substitutions are those in which at least one residue in the amino acid sequence has been removed and a different residue inserted in its place. Such substitutions may be conservative with little effect on the function of the gene, for example by substituting alanines for serines, arginines for lysines, glutamate for aspartate and the like. The substitutions which are not conservative are expected to produce the greatest changes in protein properties will be those in which (a) a hydrophilic residue, e.g., seryl or threonyl, is substituted for (or by) a hydrophobic residue, e.g., leucyl, isoleucyl, phenylalanyl, valyl or alanyl; (b) a cysteine or proline is substituted for (or by) any other residue; (c) a residue having an electropositive side chain, e.g., lysyl, arginyl, or histidyl, is substituted for (or by) an electronegative residue, e.g., glutamyl or aspartyl; or (d) a residue having a bulky side chain, e.g., phenylalanine, is substituted for (or by) one not having a side chain, e.g., glycine.

Additionally, the term “homologous sequence” may encompass a polypeptide sequence that is modified by chemical or enzymatic means. The homologous sequence may be a sequence modified by lipids, sugars, peptides, organic or inorganic compounds, by the

use of modified amino acids or the like. Protein modification techniques are illustrated in Ausubel et al. (eds) *Current Protocols in Molecular Biology*, John Wiley & Sons (1998).

Homologous sequences also may mean two sequences having a substantial percentage of sequence identity after alignment as determined by using sequence analysis programs for database searching and sequence alignment and comparison available, for example, from the Wisconsin Package Version 10.0, such as BLAST, FASTA, PILEUP, FINDPATTERNS or the like (GCG, Madision, WI). Public sequence databases such as GenBank, EMBL, Swiss-Prot and PIR or private sequence databases such as PhytoSeq (Incyte Pharmaceuticals, Palo Alto, CA) may be searched. Alignment of sequences for comparison may be conducted by the local homology algorithm of Smith and Waterman (1981) *Adv. Appl. Math.* 2:482, by the homology alignment algorithm of Needleman and Wunsch (1970) *J. Mol. Biol.* 48:443, by the search for similarity method of Pearson and Lipman (1988) *Proc. Natl. Acad. Sci. U.S.A.* 85: 2444, by computerized implementations of these algorithms. After alignment, sequence comparisons between two (or more) polynucleotides or polypeptides are typically performed by comparing sequences of the two sequences over a comparison window to identify and compare local regions of sequence similarity. The comparison window may be a segment of at least about 20 contiguous positions, usually about 50 to about 200, more usually about 100 to about 150 contiguous positions. A description of the method is provided in Ausubel et al. (eds) (1999) *Current Protocols in Molecular Biology*, John Wiley & Sons.

Transcription factors that are homologs of the disclosed sequences will typically share at least 40% amino acid sequence identity. More closely related TFs may share at least 50%, 60%, 65%, 70%, 75% or 80% sequence identity with the disclosed sequences. Factors that are most closely related to the disclosed sequences share at least 85%, 90% or 95% sequence identity. At the nucleotide level, the sequences will typically share at least 40% nucleotide sequence identity, preferably at least 50%, 60%, 70% or 80% sequence identity, and more preferably 85%, 90%, 95% or 97% sequence identity. The degeneracy of the genetic code enables major variations in the nucleotide sequence of a polynucleotide while maintaining the amino acid sequence of the encoded protein.

One way to identify whether two nucleic acid molecules are closely related is that the two molecules hybridize to each other under stringent conditions. Generally, stringent conditions are selected to be about 5°C to 20°C lower than the thermal melting point (Tm) for the specific sequence at a defined ionic strength and pH. The T_m is the temperature (under defined ionic strength and pH) at which 50% of the target sequence hybridizes to a perfectly matched probe. Conditions for nucleic acid hybridization and calculation of stringencies can be found in Sambrook et al. (1989) *Molecular Cloning. A Laboratory Manual*, Ed. 2, Cold Spring Harbor Laboratory Press, New York and Tijssen (1993) *Laboratory Techniques in Biochemistry and*

Molecular Biology--Hybridization with Nucleic Acid Probes Part I, Elsevier, New York . Nucleic acid molecules that hybridize under stringent conditions will typically hybridize to a probe based on either the entire cDNA or selected portions of the cDNA under wash conditions of 0.2x SSC to 2.0 x SSC, 0.1% SDS at 50-65° C, for example 0.2 x SSC, 0.1% SDS at 65° C. For detecting less closely related homologs washes may be performed at 50° C.

For conventional hybridization the hybridization probe is conjugated with a detectable label such as a radioactive label, and the probe is preferably of at least 20 nucleotides in length. As is well known in the art, increasing the length of hybridization probes tends to give enhanced specificity. The labeled probe derived from the *Arabidopsis* nucleotide sequence may be hybridized to a plant cDNA or genomic library and the hybridization signal detected using means known in the art. The hybridizing colony or plaque (depending on the type of library used) is then purified and the cloned sequence contained in that colony or plaque isolated and characterized. Homologs may also be identified by PCR-based techniques, such as inverse PCR or RACE, using degenerate primers. See Ausubel et al. (eds) (1998) *Current Protocols in Molecular Biology*, John Wiley & Sons.

TF homologs may alternatively be obtained by immunoscreening an expression library. With the provision herein of the disclosed TF nucleic acid sequences, the polypeptide may be expressed and purified in a heterologous expression system (e.g., *E. coli*) and used to raise antibodies (monoclonal or polyclonal) specific for the TF. Antibodies may also be raised against synthetic peptides derived from TF amino acid sequences. Methods of raising antibodies are well known in the art and are described in Harlow and Lane (1988) *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, New York. Such antibodies can then be used to screen an expression library produced from the plant from which it is desired to clone the TF homolog, using the methods described above. The selected cDNAs may be confirmed by sequencing and enzymatic activity.

3. Altered Expression of Transcription Factors

Any of the identified sequences may be incorporated into a cassette or vector for expression in plants. A number of expression vectors suitable for stable transformation of plant cells or for the establishment of transgenic plants have been described including those described in Weissbach and Weissbach, (1989) *Methods for Plant Molecular Biology*, Academic Press, and Gelvin et al., (1990) *Plant Molecular Biology Manual*, Kluwer Academic Publishers. Specific examples include those derived from a Ti plasmid of *Agrobacterium tumefaciens*, as well as those disclosed by Herrera-Estrella, L., et al., (1983) *Nature* 303: 209, Bevan, M., *Nucl. Acids Res.* (1984) 12: 8711-8721, Klee, H. J., (1985) *Bio/Technology* 3: 637-642, for dicotyledonous plants. Ti-derived plasmids can be transferred into both

monocotonous and docotyledonous species using Agrobacterium-mediated transformation (Ishida et al (1996) *Nat. Biotechnol.* 14:745-50; Barton et al. (1983) *Cell* 32:1033-1043).

Alternatively, non-Ti vectors can be used to transfer the DNA into plants and cells by using free DNA delivery techniques. Such methods may involve, for example, the use of liposomes, electroporation, microprojectile bombardment, silicon carbide wiskers, and viruses. By using these methods transgenic plants such as wheat, rice (Christou, P., (1991) *Bio/Technology* 9: 957-962) and corn (Gordon-Kamm, W., (1990) *Plant Cell* 2: 603-618) can be produced. An immature embryo can also be a good target tissue for monocots for direct DNA delivery techniques by using the particle gun (Weeks, T. et al., (1993) *Plant Physiol.* 102: 1077-1084; Vasil, V., (1993) *Bio/Technology* 10: 667-674; Wan, Y. and Lemeaux, P., (1994) *Plant Physiol.* 104: 37-48, and for *Agrobacterium*-mediated DNA transfer (Ishida et al., (1996) *Nature Biotech.* 14: 745-750).

Typically, plant transformation vectors include one or more cloned plant coding sequences (genomic or cDNA) under the transcriptional control of 5' and 3' regulatory sequences and a dominant selectable marker. Such plant transformation vectors typically also contain a promoter (*e.g.*, a regulatory region controlling inducible or constitutive, environmentally-or developmentally-regulated, or cell- or tissue-specific expression), a transcription initiation start site, an RNA processing signal (such as intron splice sites), a transcription termination site, and/or a polyadenylation signal.

Examples of constitutive plant promoters which may be useful for expressing the TF sequence include: the cauliflower mosaic virus (CaMV) 35S promoter, which confers constitutive, high-level expression in most plant tissues (*see, e.g.*, Odel et al., (1985) *Nature* 313:810); the nopaline synthase promoter (An et al., (1988) *Plant Physiol.* 88:547); and the octopine synthase promoter (Fromm et al., (1989) *Plant Cell* 1: 977).

A variety of plant gene promoters that regulate gene expression in response to environmental, hormonal, chemical, developmental signals, and in a tissue-active manner can be used for expression of the TFs in plants, as illustrated by seed-specific promoters (such as the napin, phaseolin or DC3 promoter described in US Pat. No. 5,773,697), root-specific promoters, such as those disclosed in US Patent Nos. 5,618,988, 5,837,848 and 5,905,186; fruit-specific promoters that are active during fruit ripening (such as the dru 1 promoter (US Pat. No. 5,783,393), or the 2A11 promoter (US Pat. No. 4,943,674) and the tomato polygalacturonase promoter (Bird et al. (1988) *Plant Mol. Biol.* 11:651), root-specific promoters, such as those disclosed in US Patent Nos. 5,618,988, 5,837,848 and 5,905,186, pollen-active promoters such as PTA29, PTA26 and PTA13 (US Pat. No. 5,792,929), promoters active in vascular tissue (Ringli and Keller (1998) *Plant Mol. Biol.* 37:977-988), flower-specific (Kaiser et al, (1995) *Plant Mol. Biol.* 28:231-243), pollen (Baerson et al. (1994) *Plant Mol. Biol.* 26:1947-1959), carpels (Ohl et al. (1990) *Plant Cell* 2:837-848), pollen and

ovules (Baerson et al. (1993) *Plant Mol. Biol.* 22:255-267)auxin-inducible promoters (such as that described in van der Kop et al (1999) *Plant Mol. Biol.* 39:979-990 or Baumann et al. (1999) *Plant Cell* 11:323-334), cytokinin-inducible promoter (Guevara-Garcia (1998) *Plant Mol. Biol.* 38:743-753), promoters responsive to gibberellin (Shi et al. (1998) *Plant Mol. Biol.* 38:1053-1060, Willmott et al. (1998) 38:817-825) and the like. Additional promoters are those that elicit expression in response to heat (Ainley, et al. (1993) *Plant Mol. Biol.* 22: 13-23), light (*e.g.*, the pea rbcS-3A promoter, Kuhlemeier et al., (1989) *Plant Cell* 1:471, and the maize rbcS promoter, Schaffner and Sheen, (1991) Plant *Cell* 3: 997); wounding (*e.g.*, *wunI*, Siebertz et al., (1989) *Plant Cell* 1: 961); pathogen resistance, and chemicals such as methyl jasmonate or salicylic acid (Gatz et al., (1997) *Plant Mol. Biol.* 48: 89-108). In addition, the timing of the expression can be controlled by using promoters such as those acting at late seed development (Odell et al. (1994) *Plant Physiol.* 106:447-458).

Plant expression vectors may also include RNA processing signals that may be positioned within, upstream or downstream of the coding sequence. In addition, the expression vectors may include additional regulatory sequences from the 3'-untranslated region of plant genes, *e.g.*, a 3' terminator region to increase mRNA stability of the mRNA, such as the PI-II terminator region of potato or the octopine or nopaline synthase 3' terminator regions.

Finally, as noted above, plant expression vectors may also include dominant selectable marker genes to allow for the ready selection of transformants. Such genes include those encoding antibiotic resistance genes (*e.g.*, resistance to hygromycin, kanamycin, bleomycin, G418, streptomycin or spectinomycin) and herbicide resistance genes (*e.g.*, phosphinothricin acetyltransferase).

A reduction of TF expression in a transgenic plant to modifiy a plant trait may be obtained by introducing into plants antisense constructs based on the TF cDNA. For antisense suppression, the TF cDNA is arranged in reverse orientation relative to the promoter sequence in the expression vector. The introduced sequence need not be the full length TF cDNA or gene, and need not be identical to the TF cDNA or a gene found in the plant type to be transformed. Generally, however, where the introduced sequence is of shorter length, a higher degree of homology to the native TF sequence will be needed for effective antisense suppression. Preferably, the introduced antisense sequence in the vector will be at least 30 nucleotides in length, and improved antisense suppression will typically be observed as the length of the antisense sequence increases. Preferably, the length of the antisense sequence in the vector will be greater than 100 nucleotides. Transcription of an antisense construct as described results in the production of RNA molecules that are the reverse complement of mRNA molecules transcribed from the endogenous TF gene in the plant cell. Suppression of endogenous TF gene expression can also be achieved using a ribozyme. Ribozymes are

synthetic RNA molecules that possess highly specific endoribonuclease activity. The production and use of ribozymes are disclosed in U.S. Patent No. 4,987,071 to Cech and U.S. Patent No. 5,543,508 to Haselhoff. The inclusion of ribozyme sequences within antisense RNAs may be used to confer RNA cleaving activity on the antisense RNA, such that endogenous mRNA molecules that bind to the antisense RNA are cleaved, which in turn leads to an enhanced antisense inhibition of endogenous gene expression.

Vectors in which RNA encoded by the TF cDNA (or variants thereof) is over-expressed may also be used to obtain co-suppression of the endogenous TF gene in the manner described in U.S. Patent No. 5,231,020 to Jorgensen. Such co-suppression (also termed sense suppression) does not require that the entire TF cDNA be introduced into the plant cells, nor does it require that the introduced sequence be exactly identical to the endogenous TF gene. However, as with antisense suppression, the suppressive efficiency will be enhanced as (1) the introduced sequence is lengthened and (2) the sequence similarity between the introduced sequence and the endogenous TF gene is increased.

Vectors expressing an untranslatable form of the TF mRNA may also be used to suppress the expression of endogenous TF activity to modify a trait. Methods for producing such constructs are described in U.S. Patent No. 5,583,021 to Dougherty et al. Preferably, such constructs are made by introducing a premature stop codon into the TF gene. Alternatively, a plant trait may be modified by gene silencing using double-strand RNA (Sharp (1999) *Genes and Development* 13: 139-141).

Another method for abolishing the expression of a gene is by insertion mutagenesis using the T-DNA of *Agrobacterium tumefaciens*. After generating the insertion mutants, the mutants can be screened to identify those containing the insertion in a TF gene. Mutants containing a single mutation event at the desired gene may be crossed to generate homozygous plants for the mutation (Koncz et al. (1992) *Methods in Arabidopsis Research*. World Scientific).

A plant trait may also be modified by using the cre-lox system (for example, as described in US Pat. No. 5,658,772). A plant genome may be modified to include first and second lox sites that are then contacted with a Cre recombinase. If the lox sites are in the same orientation, the intervening DNA sequence between the two sites is excised. If the lox sites are in the opposite orientation, the intervening sequence is inverted.

The polynucleotides and polypeptides of this invention may also be expressed in a plant in the absence of an expression cassette by manipulating the activity or expression level of the endogenous gene by other means. For example, by ectopically expressing a gene by T-DNA activation tagging (Ichikawa et al., (1997) *Nature* 390 698-701, Kakimoto et al., (1996) *Science* 274: 982-985). This method entails transforming a plant with a gene tag containing multiple transcriptional enhancers and once the tag has inserted into the genome, expression of a flanking gene coding sequence becomes deregulated. In another example, the

transcriptional machinery in a plant may be modified so as to increase transcription levels of a polynucleotide of the invention (See PCT Publications WO9606166 and WO 9853057 which describe the modification of the DNA binding specificity of zinc finger proteins by changing particular amino acids in the DNA binding motif).

The transgenic plant may also comprise the machinery necessary for expressing or altering the activity of a polypeptide encoded by an endogenous gene, for example by altering the phosphorylation state of the polypeptide to maintain it in an activated state.

4. Transgenic Plants with Modified TF Expression

Once an expression cassette comprising a polynucleotide encoding a TF gene of this invention has been constructed, standard techniques may be used to introduce the polynucleotide into a plant in order to modify a trait of the plant. The plant may be any higher plant, including gymnosperms, monocotyledonous and dicotyledenous plants. Suitable protocols are available for *Leguminosae* (alfalfa, soybean, clover, etc.), *Umbelliferae* (carrot, celery, parsnip), *Cruciferae* (cabbage, radish, rapeseed, broccoli, etc.), *Curcurbitaceae* (melons and cucumber), *Gramineae* (wheat, corn, rice, barley, millet, etc.), *Solanaceae* (potato, tomato, tobacco, peppers, etc.), and various other crops. See protocols described in Ammirato et al. (1984) *Handbook of Plant Cell Culture –Crop Species.* Macmillan Publ. Co. Shimamoto et al. (1989) *Nature* 338:274-276; Fromm et al. (1990) *Bio/Technology 8:833-*839; and Vasil et al. (1990) *Bio/Technology* 8:429-434.

Transformation and regeneration of both monocotyledonous and dicotyledonous plant cells is now routine, and the selection of the most appropriate transformation technique will be determined by the practitioner. The choice of method will vary with the type of plant to be transformed; those skilled in the art will recognize the suitability of particular methods for given plant types. Suitable methods may include, but are not limited to: electroporation of plant protoplasts; liposome-mediated transformation; polyethylene glycol (PEG) mediated transformation; transformation using viruses; micro-injection of plant cells; micro-projectile bombardment of plant cells; vacuum infiltration; and *Agrobacterium tumeficiens* mediated transformation. Transformation means introducing a nucleotide sequence in a plant in a manner to cause stable or transient expression of the sequence.

Successful examples of the modification of plant characteristics by transformation with cloned sequences which serve to illustrate the current knowledge in this field of technology, and which are herein incorporated by reference, include: U.S. Patent Nos. 5,571,706; 5,677,175; 5,510,471; 5,750,386; 5,597,945; 5,589,615; 5,750,871; 5,268,526; 5,780,708; 5,538,880; 5,773,269; 5,736,369 and 5,610,042.

Following transformation, plants are preferably selected using a dominant selectable marker incorporated into the transformation vector. Typically, such a marker will confer

antibiotic or herbicide resistance on the transformed plants, and selection of transformants can be accomplished by exposing the plants to appropriate concentrations of the antibiotic or herbicide.

After transformed plants are selected and grown to maturity, those plants showing a modified trait are identified. The modifed trait may be any of those traits described above. Additionally, to confirm that the modified trait is due to changes in expression levels or activity of the polypeptide or polynucleotide of the invention may be determined by analyzing mRNA expression using Northern blots, RT-PCR or microarrays, or protein expression using immunoblots or Western blots or gel shift assays.

The plants may have commercial utility for increasing tolerance or resistance to pathogens and pests. These transgenic plants may be more resistant to biotrophic or necrotrophic pathogens or belonging to the following groups such as a fungus, bacterium, mollicute, virus, nematode, a parasitic higher plant or the like and associated diseases. In particular, pathogens such as *Fusarium oxysporum*, *Erysyphe orontii* and other powdery mildews, *Sclerotinia spp.*, soil-borne oomycetes, foliar oomycetes, *Botrytis spp.*, *Rhizoctonia spp*, *Verticillium dahliae/albo-atrum*, *Alternaria spp.*, rusts, *Mycosphaerella spp*, *Fusarium solani*, or the like. The diseases include fungal diseases such as rusts, smuts, wilts, yellows, root rot, leaf drop, ergot, leaf blight of potato, brown spot of rice, leaf blight, late blight, powdery mildew, downy mildew, and the like; viral diseases such as sugarcane mosaic, cassava mosaic, sugar beet yellows, plum pox, barley yellow dwarf, tomato yellow leaf curl, tomato spotted wilt virus, and the like; bacterial diseases such as citrus canker, bacterial leaf blight, bacterial will, soft rot of vegetables, and the like; nematode diseases caused by parasitic nematodes such as root-knot nematodes, cyst nematodes or the like.

5. Other Utility of the Polypeptide and Polynucleotide Sequences

A transcription factor provided by the present invention may also be used to identify exogenous or endogenous molecules that may affect expression of the transcription factors and may affect any of the traits described herein. These molecules may include organic or inorganic compounds.

For example, the method may entail first placing the molecule in contact with a plant or plant cell. The molecule may be introduced by topical administration, such as spraying or soaking of a plant, and then the molecule's effect on the expression or activity of the TF polypeptide or the expression of the polynucleotide monitored. Changes in the expression of the TF polypeptide may be monitored by use of polyclonal or monoclonal antibodies, gel electrophoresis or the like. Changes in the expression of the corresponding polynucleotide sequence may be detected by use of microarrays, Northerns or any other technique for monitoring changes in mRNA expression. These techniques are exemplified in Ausubel et al.

(eds) *Current Protocols in Molecular Biology*, John Wiley & Sons (1998). Such changes in the expression levels may be correlated with modified plant traits and thus identified molecules may be useful for soaking or spraying on fruit, vegetable and grain crops to modify traits in plants.

The transcription factors may also be employed to identify promoter sequences with which they may interact. After identifying a promoter sequence, interactions between the transcription factor and the promoter sequence may be modified by changing specific nucleotides in the promoter sequence or specific amino acids in the transcription factor that interact with the promoter sequence to alter a plant trait. Typically, transcription factor DNA binding sites are identified by gel shift assays. After identifying the promoter regions, the promoter region sequences may be employed in double-stranded DNA arrays to identify molecules that affect the interactions of the TFs with their promoters (Bulyk et al. (1999) *Nature Biotechnology* 17:573-577).

The identified transcription factors are also useful to identify proteins that modify the activity of the transcription factor. Such modification may occur by covalent modification, such as by phosphorylation, or by protein-protein (homo or-heteropolymer) interactions. Any method suitable for detecting protein-protein interactions may be employed. Among the methods that may be employed are co-immunoprecipitation, cross-linking and co-purification through gradients or chromatographic columns, and the two-hybrid yeast system.

The two-hybrid system detects protein interactions in vivo and is described in Chien, et al., (1991), *Proc. Natl. Acad. Sci. USA*, 88, 9578-9582 and is commercially available from Clontech (Palo Alto, Calif.). In such a system, plasmids are constructed that encode two hybrid proteins: one consists of the DNA-binding domain of a transcription activator protein fused to the TF polypeptide and the other consists of the transcription activator protein's activation domain fused to an unknown protein that is encoded by a cDNA that has been recombined into the plasmid as part of a cDNA library. The DNA-binding domain fusion plasmid and the cDNA library are transformed into a strain of the yeast *Saccharomyces cerevisiae* that contains a reporter gene (e.g., lacZ) whose regulatory region contains the transcription activator's binding site. Either hybrid protein alone cannot activate transcription of the reporter gene. Interaction of the two hybrid proteins reconstitutes the functional activator protein and results in expression of the reporter gene, which is detected by an assay for the reporter gene product. Then, the library plasmids responsible for reporter gene expression are isolated and sequenced to identify the proteins encoded by the library plasmids. After identifying proteins that interact with the transcription factors, assays for compounds that interfere with the TF protein-protein interactions may be preformed.

The following examples are intended to illustrate but not limit the present invention.

Example I. Full Length Gene Identification and Cloning

Putative transcription factor sequences (genomic or ESTs) related to known transcription factors were identified in the *Arabidopsis thaliana* GenBank database using the tblastn sequence analysis program using default parameters and a P-value cutoff threshold of –4 or –5 or lower, depending on the length of the query sequence. Putative transcription factor sequence hits were then screened to identify those containing particular sequence strings. If the sequence hits contained such sequence strings, the sequences were confirmed as transcription factors.

Alternatively, *Arabidopsis thaliana* cDNA libraries derived from different tissues or treatments, or genomic libraries were screened to identify novel members of a transcription family using a low stringency hybridization approach. Probes were synthesized using gene specific primers in a standard PCR reaction (annealing temperature 60° C) and labeled with ^{32}P dCTP using the High Prime DNA Labeling Kit (Boehringer Mannheim). Purified radiolabelled probes were added to filters immersed in Church hybridization medium (0.5 M $NaPO_4$ pH 7.0, 7% SDS, 1 % w/v bovine serum albumin) and hybridized overnight at 60 °C with shaking. Filters were washed two times for 45 to 60 minutes with 1xSCC, 1% SDS at 60° C.

To identify additional sequence 5' or 3' of a partial cDNA sequence in a cDNA library, 5' and 3' rapid amplification of cDNA ends (RACE) was performed using the Marathon™ cDNA amplification kit (Clontech, Palo Alto, CA). Generally, the method entailed first isolating poly(A) mRNA, performing first and second strand cDNA synthesis to generate double stranded cDNA, blunting cDNA ends, followed by ligation of the Marathon™ Adaptor to the cDNA to form a library of adaptor-ligated ds cDNA. Gene-specific primers were designed to be used along with adaptor specific primers for both 5' and 3' RACE reactions. Nested primers, rather than single primers, were used to increase PCR specificity. Using 5' and 3' RACE reactions, 5' and 3' RACE fragments were obtained, sequenced and cloned. The process may be repeated until 5' and 3' ends of the full-length gene were identified. Then the full-length cDNA was generated by PCR using primers specific to 5' and 3' ends of the gene by end-to-end PCR.

Example II Pathogen Resistance Genes

RT-PCR and microarray experiments were performed to identify those genes induced after exposure to biotropic fungal pathogens, such as *Erisyphe orontii*, necrotropic fungal pathogens, such as *Fusarium oxysporum*, and disease associated growth-regulators such as salicylic acid, methyl jasmonate and ethylene (ACC). The gene expression patterns from soil grown as well as tissue culture grown plant tissue were investigated.

Fusarium oxysporum isolates cause vascular wilts and damping off of various annual vegetables, perennials and weeds (Mauch-Mani and Slusarenko (1994) Molecular Plant-Microbe Interactions 7: 378-383). For *Fusarium oxysporum* experiments, plants grown on petri dishes were sprayed with a fresh spore suspension of *F. oxysporum*. The spore suspension was prepared as follows: A plug of fungal hyphae from a plate culture was placed on a fresh potato dextrose agar plate and allowed to spread for one week. 5 ml sterile water was then added to the plate, swirled, and pipetted into 50 ml Armstrong Fusarium medium. Spores were grown overnight in Fusarium medium and then sprayed onto plants using a Preval paint sprayer. Plant tissue was harvested and frozen in liquid nitrogen 48 hours post infection

Erysiphe orontii is a causal agent of powdery mildew. For *Erysiphe orontii* experiments, plants were grown approximately 4 weeks in a greenhouse under 12 hour light (20 C, ~30% relative humidity (rh)). Individual leaves were infected with *E. orontii* spores from infected plants using a camel's hair brush, and the plants were transferred to a Percival growth chamber (20 C, 80% rh.). Plant tissue was harvested and frozen in liquid nitrogen 7 days post infection.

For salicylic acid experiments, 15 day old seedlings grown on petri dishes were transferred to plates containing 0.5 mM salicylic acid (SA). After 72 hours, leaves were harvested and frozen in liquid nitrogen.

Reverse transcriptase PCR was done using gene specific primers within the coding region for each sequence identified. The primers were designed near the 3' region of each coding sequence initially identified.

Total RNA from these tissues were isolated using the CTAB extraction protocol. Once extracted total RNA was normalized in concentration across all the tissue types to ensure that the PCR reaction for each tissue received the same amount of cDNA template using the 28S band as reference. Poly A+ was purified using a modified protocol from the Qiagen Oligotex kit batch protocol. cDNA was synthesized using standard protocols. After the first strand cDNA synthesis, primers for Actin 2 were used to normalize the concentration of cDNA across the tissue types. Actin 2 is found to be constitutively expressed in fairly equal levels across the tissue types we are investigating.

For RT PCR, cDNA template was mixed with corresponding primers and Taq polymerase. Each reaction consisted of 0.2 ul cDNA template, 2ul 10X Tricine buffer, 2 ul 10X Tricine buffer and 16.8 ul water, 0.05ul Primer 1, 0.05 ul, Primer 2, 0.3 ul Taq polymerase and 8.6 ul water.

The 96 well plate was covered with microfilm and set in the Thermocycler to start the following reaction cycle. Step1 93° C for 3 mins, Step 2 93° C for 30 sec, Step 3 65° C for 1 min, Step 4 72° C for 2 mins,. Steps 2, 3 and 4 were repeated for 28 cycles, Step 5 72° C

for 5 mins and Step 6 4° C. The PCR plate was placed back in the thermocycler to amplify more products at 8 more cycles to identify genes that have very low expression. The reaction cycle was as follows: Step 2 93° C for 30 sec, Step 3 65° C for 1 min, and Step 4 72° C for 2 ins, repeated for 8 cycles, and Step 4 4° C.

8ul of PCR product and 1.5 ul of loading dye were loaded on a 1.2% agarose gel for analysis after 28 cycles and 36 cycles. Expression levels of specific transcripts were considered low if they were only detectable after 36 cycles of PCR. Expression levels were considered medium or high depending on the levels of transcript compared with observed transcript levels for actin2.

In some instances, expression patterns of the transcription factors was monitored by microarray experiments. cDNAs were generated by PCR and resuspended at a final concentration of ~ 100 ng/ul in 3X SSC or 150mM Na-phosphate (Eisen and Brown (1999) *Meth. in Enzymol.* 303:179-205). The cDNAs were spotted on microscope glass slides coated with polylysine. The prepared cDNAs were aliquoted into 384 well plates and spotted on the slides using an x-y-z gantry (OmniGrid) purchased from GeneMachines (Menlo Park, CA) outfitted with quill type pins purchased from Telechem International (Sunnyvale, CA). After spotting, the arrays were cured for a minimum of one week at room temperature, rehydrated and blocked following the protocol recommended by Eisen and Brown (1999).

Sample total RNA (10 ug) samples were labeled using fluorescent Cy3 and Cy5 dyes. Labeled samples were resuspended in 4X SSC/0.03% SDS/4 ug salmon sperm DNA/2 ug tRNA/ 50mM Na-pyrophosphate, heated for 95°C for 2.5 minutes, spun down and placed on the array. The array was then covered with a glass coverslip and placed in a sealed chamber. The chamber was then kept in a water bath at 62°C overnight. The arrays were washed as described in Eisen and Brown (1999) and scanned on a General Scanning 3000 laser scanner. The resulting files are subsequently quantified using Imagene a software purchased from BioDiscovery (Los Angeles, CA).

The transcript levels were observed to be upregulated between 1.5 and 100 fold when compared with control plants not exposed to the pathogens.

Example III. Construction of Expression Vectors

The sequence was amplified from a genomic or cDNA library using primers specific to sequences upstream and downstream of the coding region. The expression vector was pMEN20, which is derived from pMON316 (Sanders et al, (1987) *Nucleic Acids Research* 15:1543-58). To clone the sequence into the vector, both pMEN20 and the amplified DNA fragment were digested separately with SalI and NotI restriction enzymes at 37° C for 2 hours. The digestion products were subject to electrophoresis in a 0.8% agarose gel and visualized

by ethidium bromide staining. The DNA fragments containing the sequence and the linearized plasmid were excised and purified by using a Qiaquick gel extraction kit (Qiagen, CA). The fragments of interest were ligated at a ratio of 3:1 (vector to insert). Ligation reactions using T4 DNA ligase (New England Biolabs, MA) were carried out at 16° C for 16 hours. The ligated DNAs were transformed into competent cells of the *E. coli* strain DH5alpha by using the heat shock method. The transformations were plated on LB plates containing 50 mg/l spectinomycin (Sigma).

Individual colonies were grown overnight in five milliliters of LB broth containing 50 mg/l spectinomycin at 37° C. Plasmid DNA was purified by using Qiaquick Mini Prep kits (Qiagen, CA).

Example IV. Transformation of *Agrobacterium* with the Expression Vector

After the plasmid vector containing the gene was constructed, the vector was used to transform *Agrobacterium tumefaciens* cells expressing the gene products. The stock of *Agrobacterium tumefaciens* cells for transformation were made as described by Nagel et al. *FEMS Microbiol Letts* 67: 325-328 (1990). *Agrobacterium* strain GV3101 was grown in 250 ml LB medium (Sigma) overnight at 28°C with shaking until an absorbance (A_{600}) of 0.5 – 1.0 was reached. Cells were harvested by centrifugation at 4,000 x g for 15 min at 4° C. Cells were then resuspended in 250 μl chilled buffer (1 mM HEPES, pH adjusted to 7.0 with KOH). Cells were centrifuged again as described above and resuspended in 125 μl chilled buffer. Cells were then centrifuged and resuspended two more times in the same HEPES buffer as described above at a volume of 100 μl and 750 μl, respectively. Resuspended cells were then distributed into 40 μl aliquots, quickly frozen in liquid nitrogen, and stored at -80° C.

Agrobacterium cells were transformed with plasmids prepared as described above following the protocol described by Nagel et al. *FEMS Microbiol Letts* 67: 325-328 (1990). For each DNA construct to be transformed, 50 – 100 ng DNA (generally resuspended in 10 mM Tris-HCl, 1 mM EDTA, pH 8.0) was mixed with 40 μl of *Agrobacterium* cells. The DNA/cell mixture was then transferred to a chilled cuvette with a 2mm electrode gap and subject to a 2.5 kV charge dissipated at 25 μF and 200 μF using a Gene Pulser II apparatus (Bio-Rad). After electroporation, cells were immediately resuspended in 1.0 ml LB and allowed to recover without antibiotic selection for 2 – 4 hours at 28° C in a shaking incubator. After recovery, cells were plated onto selective medium of LB broth containing 100 μg/ml spectinomycin (Sigma) and incubated for 24-48 hours at 28° C. Single colonies were then picked and inoculated in fresh medium. The presence of the plasmid construct was verified by PCR amplification and sequence analysis.

Example V. Transformation of *Arabidopsis* Plants with *Agrobacterium tumefaciens* with Expression Vector

After transformation of *Agrobacterium tumefaciens* with plasmid vectors containing the gene, single *Agrobacterium* colonies were identified, propagated, and used to transform *Arabidopsis* plants. Briefly, 500 ml cultures of LB medium containing 50 mg/l spectinomycin were inoculated with the colonies and grown at 28° C with shaking for 2 days until an absorbance (A_{600}) of > 2.0 is reached. Cells were then harvested by centrifugation at 4,000 x g for 10 min, and resuspended in infiltration medium (1/2 X Murashige and Skoog salts (Sigma), 1 X Gamborg's B-5 vitamins (Sigma), 5.0% (w/v) sucrose (Sigma), 0.044 μM benzylamino purine (Sigma), 200 μl/L Silwet L-77 (Lehle Seeds) until an absorbance (A_{600}) of 0.8 was reached.

Prior to transformation, *Arabidopsis thaliana* seeds (ecotype Columbia) were sown at a density of ~10 plants per 4" pot onto Pro-Mix BX potting medium (Hummert International) covered with fiberglass mesh (18 mm X 16 mm). Plants were grown under continuous illumination (50-75 $\mu E/m^2/sec$) at 22-23° C with 65-70% relative humidity. After about 4 weeks, primary inflorescence stems (bolts) are cut off to encourage growth of multiple secondary bolts. After flowering of the mature secondary bolts, plants were prepared for transformation by removal of all siliques and opened flowers.

The pots were then immersed upside down in the mixture of *Agrobacterium* infiltration medium as described above for 30 sec, and placed on their sides to allow draining into a 1' x 2' flat surface covered with plastic wrap. After 24 h, the plastic wrap was removed and pots are turned upright. The immersion procedure was repeated one week later, for a total of two immersions per pot. Seeds were then collected from each transformation pot and analyzed following the protocol described below.

Example VI. Identification of Arabidopsis Primary Transformants

Seeds collected from the transformation pots were sterilized essentially as follows. Seeds were dispersed into in a solution containing 0.1% (v/v) Triton X-100 (Sigma) and sterile H_2O and washed by shaking the suspension for 20 min. The wash solution was then drained and replaced with fresh wash solution to wash the seeds for 20 min with shaking. After removal of the second wash solution, a solution containing 0.1% (v/v) Triton X-100 and 70% ethanol (Equistar) was added to the seeds and the suspension was shaken for 5 min. After removal of the ethanol/detergent solution, a solution containing 0.1% (v/v) Triton X-100 and 30% (v/v) bleach (Clorox) was added to the seeds, and the suspension was shaken for 10 min. After removal of the bleach/detergent solution, seeds were then washed five times in sterile distilled H_2O. The seeds were stored in the last wash water at 4° C for 2 days in the dark before being plated onto antibiotic selection medium (1 X Murashige and Skoog salts (pH

adjusted to 5.7 with 1M KOH), 1 X Gamborg's B-5 vitamins, 0.9% phytagar (Life Technologies), and 50 mg/l kanamycin). Seeds were germinated under continuous illumination (50-75 μE/m^2/sec) at 22-23° C. After 7-10 days of growth under these conditions, kanamycin resistant primary transformants (T_1 generation) were visible and obtained. These seedlings were transferred first to fresh selection plates where the seedlings continued to grow for 3-5 more days, and then to soil (Pro-Mix BX potting medium).

Primary transformants are self-crossed and progeny seeds (T2) collected.

Example VII. Analysis of Arabidopsis T2 progeny plants for Pathogen Resistance or Pathogen Tolerance

T2 or knockout mutant seed were surface sterilized and sown on MS media containing sucrose. Ten days post-planting, seedlings were transferred to MS media without sucrose. At two weeks of age *Arabidopsis* seedlings were inoculated with *Fusarium* by spraying with a spore suspension (2 x 10^6 conidia per milliliter) and incubated under high humidity. Plants were then scored macroscopically for disease symptoms or microscopically for fungal growth or using microarrays for the induction of resistance associated genes (such as the defensin genes) to detect resistance or tolerance of the plant tissue. A wild type plant shows the first signs of damage (gradual yellowing of leaves, damping off of seedlings or growth of fungal mycelium) after two to four days after inoculation. Transgenic plants that are pathogen resistant or tolerant showed a delay in disease or symptom development compared to wild-type control plants.

Alternatively, *Erysiphe* inoculations were done by tapping conidia from 1 to 2 heavily infected leaves onto the mesh cover of a settling tower, brushing the mesh with a camel's hair paint brush to break up the conidial chains, and letting the conidia settle for 10 minutes. Plants were 4 to 4.5 weeks old at the time of inoculation. Spores were obtained from 10 to 14 day old *Erysiphe* cultures. Typically, within the first twenty-four hours, the spores differentiated into several fungal structures including the haustorium that invaginates a host's epidermal plasma membrane. Formation of aerial mycelium and sporulation represent late differentiation events between 4 and 7 days post inoculation (Freilaldenhoven et al. (1994) *Plant Cell* 6: 983-994). Plant resistance was scored based on the relative number and size of mycelial patches bearing conidia compared to wild-type control plants. Events associated with disease resistance to the pathogens and pests include: the induction of pathogen resistance related genes (R genes), the activation of cell death in the attacked epidermal cells (hypersensitive response), the induction of anti-microbial compounds, such as phytoalexins, and the lignification that occurs at attempted penetration sites. Assays are performed to observe these events. Transgenic plants identified that induce R genes, activate cell death, induce anti-microbial compounds or increase lignification sooner or to a greater extent than

wild-type plants when exposed to pathogen are potentially more resistant to infection by Erysiphe as well as a number of other pathogens and pests.

We have observed that when the expression levels of the genes are altered, that the disease phenotype can be varied. For example, G19 was significantly induced upon infection by the fungal pathogen *Erysiphe orontii* as well as the disease associated growth regulator, ethylene. Our data show that G19 overexpressing plants were more tolerant to infection with a moderate dose of *Erysiphe orontii* and in a nematode screen. The transgenic plants overexpressing G19 under the control of the 35S promoter were morphologically similar to control plants.

Additionally, G511 was another example of a gene that when overexpressed showed an increased tolerance to the fungal pathogen *Erysiphe orontii.* In both cases increased tolerance includes a significant reduction in pathogen growth and symptom development compared to wild type plants that were treated with pathogen in an identical manner.

Example VIII. Transformation of Cereal Plants with the Expression Vector

A cereal plant, such as corn, wheat, rice, sorghum or barley, can also be transformed with the plasmid vectors containing the sequence and constitutive or inducible promoters to modify a trait. In these cases, a cloning vector, pMEN020, is modified to replace the NptII coding region with the BAR gene of *Streptomyces hygroscopicus* that confers resistance to phosphinothricin. The KpnI and BglII sites of the Bar gene are removed by site-directed mutagenesis with silent codon changes.

Plasmids according to the present invention may be transformed into corn embryogenic cells derived from immature scutellar tissue by using microprojectile bombardment, with the A188XB73 genotype as the preferred genotype (Fromm et al., *Bio/Technology* 8: 833-839 (1990); Gordon-Kamm et al., *Plant Cell* 2: 603-618 (1990)). After microprojectile bombardment the tissues are selected on phosphinothricin to identify the transgenic embryogenic cells (Gordon-Kamm et al., *Plant Cell* 2: 603-618 (1990)). Transgenic plants are regenerated by standard corn regeneration techniques (Fromm, et al., *Bio/Technology* 8: 833-839 (1990); Gordon-Kamm et al., *Plant Cell* 2: 603-618 (1990)).

Example IX. Identification of Homologous Sequences

Homologs from the same plant, different plant species or other organisms were identified using database sequence search tools, such as the Basic Local Alignment Search Tool (BLAST) (Altschul et al. (1990) *J. Mol. Biol.* 215:403-410; and Altschul et al. (1997) *Nucl. Acid Res.* 25: 3389-3402). The tblastn or blastn sequence analysis programs were employed using the BLOSUM-62 scoring matrix (Henikoff, S. and Henikoff, J. G. (1992) *Proc. Natl. Acad. Sci. USA* 89: 10915-10919). The output of a BLAST report provides a score that takes

into account the alignment of similar or identical residues and any gaps needed in order to align the sequences. The scoring matrix assigns a score for aligning any possible pair of sequences. The P values reflect how many times one expects to see a score occur by chance. Higher scores are preferred and a low threshold P value threshold is preferred. These are the sequence identity criteria. The tblastn sequence analysis program was used to query a polypeptide sequence against six-way translations of sequences in a nucleotide database. Hits with a P value less than -25, preferably less than -70, and more preferably less than -100, were identified as homologous sequences (exemplary selected sequence criteria). The blastn sequence analysis program was used to query a nucleotide sequence against a nucleotide sequence database. In this case too, higher scores were preferred and a preferred threshold P value was less than -13, preferably less than -50, and more preferably less than -100.

Alternatively, a fragment of a sequence from Figure 1 is ^{32}P-radiolabeled by random priming (Sambrook et al., (1989) *Molecular Cloning. A Laboratory Manual*, 2nd Ed., Cold Spring Harbor Laboratory Press, New York) and used to screen a plant genomic library (the exemplary test polynucleotides). As an example, total plant DNA from *Arabidopsis thaliana*, Nicotiana *tabacum*, *Lycopersicon pimpinellifolium*, Prunus *avium*, Prunus *cerasus*, Cucumis *sativus*, or *Oryza sativa* are isolated according to Stockinger al (Stockinger, E. J., et al., (1996), *J. Heredity*, 87:214-218). Approximately 2 to 10 μg of each DNA sample are restriction digested, transferred to nylon membrane (Micron Separations, Westboro, MA) and hybridized. Hybridization conditions are: 42^{o} C in 50% formamide, 5X SSC, 20 mM phosphate buffer 1X Denhardt's, 10% dextran sulfate, and 100μg/ml herring sperm DNA. Four low stringency washes at RT in 2X SSC, 0.05% sodium sarcosyl and 0.02% sodium pyrophosphate are performed prior to high stringency washes at 55^{o} C in 0.2X SSC, 0.05% sodium sarcosyl and 0.01% sodium pyrophosphate. High stringency washes are performed until no counts are detected in the washout according to Walling et al. (Walling, L. L., et al., (1988) Nucl. Acids Res. 16:10477-10492).

All references (publications and patents) are incorporated herein by reference in their entirety for all purposes.

Although the invention has been described with reference to the embodiments and examples above, it should be understood that various modifications can be made without departing from the spirit of the invention. Accordingly, the invention is limited only by the following claims.

We Claim:

1. A transgenic plant comprising a recombinant polynucleotide comprising a nucleotide sequence encoding a polypeptide comprising at least 6 consecutive amino acids of a sequence selected from the group consisting of SEQ ID Nos. 2N, where N=1-56, wherein the recombinant polynucleotide alters the plant's disease tolerance or resistance when compared with the same trait of another plant lacking the recombinant polynucleotide.

2. The transgenic plant of claim 1, wherein the nucleotide sequence encodes a polypeptide comprising a conserved domain selected from the group consisting of SEQ ID Nos. 2N, where N=1-56

3. The transgenic plant of claim 1, wherein the recombinant polynucleotide further comprises a promoter operably linked to said nucleotide sequence.

4. The transgenic plant of claim 3, wherein said promoter is constitutive or inducible or tissue-active.

5. A method for altering the disease tolerance or resistance of a plant, said method comprising (a) transforming a plant with a recombinant polynucleotide comprising a nucleotide sequence encoding a polypeptide comprising at least 6 consecutive amino acids of a sequence selected from the group consisting of SEQ ID Nos. 2N, where N=1-56, (b) selecting said transformed plants; and (c) identifying a transformed plant having an altered disease tolerance or resistance.

6. The method of claim 5, wherein the nucleotide sequence encodes a polypeptide comprising a conserved domain selected from the group consisting of SEQ ID Nos. 2N, where N=1-56.

8. The method of claim 5, wherein the recombinant polynucleotide further comprises a promoter operably linked to said nucleotide sequence.

9. The method of claim 8, wherein said promoter is constitutive or inducible or tissue-active.

10. A method for altering the expression levels of at least one gene in a plant, said method comprising (a) transforming the plant with a recombinant polynucleotide comprising a nucleotide sequence encoding a polypeptide comprising at least 6 consecutive amino acids of a sequence selected from the group consisting of SEQ ID Nos. 2N, where N=1-56; and (b) selecting said transformed plant.

11. The method of claim 10, wherein said recombinant polynucleotide encodes a polypeptide comprising a conserved domain selected from the group consisting of SEQ ID Nos. 2N, where N=1-56.

12. The method of claim 10, wherein the nucleotide sequence further comprises a promoter operably linked to said nucleotide sequence.

13. The method of claim 10, wherein said promoter is constitutive or inducible or tissue-active.

14. A method for altering the disease tolerance or resistance in a plant, said method comprising (a) transforming the plant with a recombinant polynucleotide comprising at least 18 consecutive nucleotides of a sequence selected from the group consisting of SEQ ID Nos. 2N-1, where N= 1-56, and SEQ ID Nos. 113-121; and (b) selecting said transformed plant.

15. A method for altering a plant's trait, said method comprising (a) providing a database sequence; (b) comparing said database sequence with a polypeptide selected from SEQ ID Nos. 2N, where N= 1-56; (c) selecting a database sequence that meets selected sequence criteria; and (d) transforming said selected database sequence in the plant.

16. A method for altering a plant's trait, said method comprising (a) providing a database sequence; (b) comparing said database sequence with a polynucleotide selected from SEQ ID Nos. 2N-1, where N= 1-56 or SEQ ID Nos. 113-121; (c) selecting a database sequence that meets selected sequence criteria; and (d) transforming said selected database sequence in the plant.

17. A method for altering a plant's trait, said method comprising (a) providing a test polynucleotide; (b) hybridizing said test polynucleotide with a polynucleotide selected from SEQ ID Nos. 2N-1, where N= 1-56 or SEQ ID Nos. 113-121 at low stringency; and (c) transforming said hybridizing test polynucleotide in a plant to alter a trait of the plant.

ABSTRACT OF THE INVENTION

Recombinant polynucleotides and methods for altering the regulation of gene expression in plants are provided to modify a plant's traits, in particular disease tolerance.

Figure 1a

SEQ ID No	GID No.	Family	Fragments	DNA or protein	coding sequence	conserved domain
1	G1043	WRKY	1-100, 30-48, 75-125, 150-200, 200-300, 350-400	DNA	43-927	
2	G1043	WRKY	1-50, 50-75, 76-81, 82-100, 100-150, 150-200	protein		120-179
3	G759	NAM	1-100, 30-48, 75-125, 150-200, 200-300, 350-400	DNA	8-961	
4	G759	NAM	1-50, 50-75, 76-81, 82-100, 100-150, 150-200	protein		17-159
5	G185	WRKY	1-100, 30-48, 75-125, 150-200, 200-300, 350-400	DNA	77-988	
6	G185	WRKY	1-50, 50-75, 76-81, 82-100, 100-150, 150-200	protein		113-172
7	G629	bZIP	1-100, 30-48, 75-125, 150-200, 200-300, 350-400	DNA	169-1275	
8	G629	bZIP	1-50, 50-75, 76-81, 82-100, 100-150, 150-200	protein		92-152
9	G435	HB	1-100, 30-48, 75-125, 150-200, 200-300, 350-400	DNA	32-502	
10	G435	HB	1-50, 50-75, 76-81, 82-100, 100-150, 150-200	protein		4-67
11	G4	AP2	1-100, 30-48, 75-125, 150-200, 200-300, 350-400	DNA	90-1217	
12	G4	AP2	1-50, 50-75, 76-81, 82-100, 100-150, 150-200	protein		121-188
13	G1035	bZIP	1-100, 30-48, 75-125, 150-200, 200-300, 350-400	DNA	103-624	
14	G1035	bZIP	1-50, 50-75, 76-81, 82-100, 100-150, 150-200	protein		39-91
15	G179	WRKY	1-100, 30-48, 75-125, 150-200, 200-300, 350-400	DNA	68-511	
16	G179	WRKY	1-50, 50-75, 76-81, 82-100, 100-150, 150-200	protein		65-121
17	G28	AP2	1-100, 30-48, 75-125, 150-200, 200-300, 350-400	DNA	63-869	
18	G28	AP2	1-50, 50-75, 76-81, 82-100, 100-150, 150-200	protein		145-213
19	G1241	MISC	1-100, 30-48, 75-125, 150-200, 200-300, 350-400	DNA	108-605	
20	G1241	MISC	1-50, 50-75, 76-81, 82-100, 100-150, 150-200	protein		
21	G19	AP2	1-100, 30-48, 75-125, 150-200, 200-300, 350-400	DNA	70-816	
22	G19	AP2	1-50, 50-75, 76-81, 82-100, 100-150, 150-200	protein		76-145
23	G503	NAM	1-100, 30-48, 75-125, 150-200, 200-300, 350-400	DNA	80-886	
24	G503	NAM	1-50, 50-75, 76-81, 82-100, 100-150, 150-200	protein		12-158
25	G263	HS	1-100, 30-48, 75-125, 150-200, 200-300, 350-400	DNA	48-902	
26	G263	HS	1-50, 50-75, 76-81, 82-100, 100-150, 150-200	protein		15-105
27	G921	WRKY	1-100, 30-48, 75-125, 150-200, 200-300, 350-400	DNA	116-1024	
28	G921	WRKY	1-50, 50-75, 76-81, 82-100, 100-150, 150-200	protein		146-203
29	G1275	WRKY	1-100, 30-48, 75-125, 150-200, 200-300, 350-400	DNA	58-579	
30	G1275	WRKY	1-50, 50-75, 76-81, 82-100, 100-150, 150-200	protein		113-169

Figure 1b

SEQ ID No	GID No.	Family	Fragments	DNA or protein	coding sequence	conserved domain
31	G242	MYB	1-100, 30-48, 75-125, 150-200, 200-300, 350-400	DNA	66-983	
32	G242	MYB	1-50, 50-75, 76-81, 82-100, 100-150, 150-200	protein		6-105
33	G1006	AP2	1-100, 30-48, 75-125, 150-200, 200-300, 350-400	DNA	52-783	
34	G1006	AP2	1-50, 50-75, 76-81, 82-100, 100-150, 150-200	protein		114-182
35	G1049	bZIP	1-100, 30-48, 75-125, 150-200, 200-300, 350-400	DNA	29-550	
36	G1049	bZIP	1-50, 50-75, 76-81, 82-100, 100-150, 150-200	protein		77-132
37	G502	NAM	1-100, 30-48, 75-125, 150-200, 200-300, 350-400	DNA	224-1186	
38	G502	NAM	1-50, 50-75, 76-81, 82-100, 100-150, 150-200	protein		10-155
39	G239	MYB	1-100, 30-48, 75-125, 150-200, 200-300, 350-400	DNA	1-822	
40	G239	MYB	1-50, 50-75, 76-81, 82-100, 100-150, 150-200	protein		21-125
41	G555	bZIP	1-100, 30-48, 75-125, 150-200, 200-300, 350-400	DNA	250-1242	
42	G555	bZIP	1-50, 50-75, 76-81, 82-100, 100-150, 150-200	protein		38-110
43	G352	Z	1-100, 30-48, 75-125, 150-200, 200-300, 350-400	DNA	80-817	
44	G352	Z	1-50, 50-75, 76-81, 82-100, 100-150, 150-200	protein		99-119,166-186
45	G1352	Z	1-100, 30-48, 75-125, 150-200, 200-300, 350-400	DNA	79-900	
46	G1352	Z	1-50, 50-75, 76-81, 82-100, 100-150, 150-200	protein		108-129,167-188
47	G1089	bZIPt2	1-100, 30-48, 75-125, 150-200, 200-300, 350-400	DNA	31-2427	
48	G1089	bZIPt2	1-50, 50-75, 76-81, 82-100, 100-150, 150-200	protein		425-500
49	G553	bZIP	1-100, 30-48, 75-125, 150-200, 200-300, 350-400	DNA	82-1236	
50	G553	bZIP	1-50, 50-75, 76-81, 82-100, 100-150, 150-200	protein		94-160
51	G1221	MISC	1-100, 30-48, 75-125, 150-200, 200-300, 350-400	DNA	287-2314	
52	G1221	MISC	1-50, 50-75, 76-81, 82-100, 100-150, 150-200	protein		490-515
53	G580	bZIP	1-100, 30-48, 75-125, 150-200, 200-300, 350-400	DNA	43-747	
54	G580	bZIP	1-50, 50-75, 76-81, 82-100, 100-150, 150-200	protein		162-218
55	G270	AKR	1-100, 30-48, 75-125, 150-200, 200-300, 350-400	DNA	43-1350	
56	G270	AKR	1-50, 50-75, 76-81, 82-100, 100-150, 150-200	protein		
57	G201	MYB	1-100, 30-48, 75-125, 150-200, 200-300, 350-400	DNA	1-1011	
58	G201	MYB	1-50, 50-75, 76-81, 82-100, 100-150, 150-200	protein		14-114
59	G1417	WRKY	1-100, 30-48, 75-125, 150-200, 200-300, 350-400	DNA	32-1501	
60	G1417	WRKY	1-50, 50-75, 76-81, 82-100, 100-150, 150-200	protein		239-296

Figure 1c

SEQ ID No	GID No.	Family	Fragments	DNA or protein	coding sequence	conserved domain
61	G233	MYB	1-100, 30-48, 75-125, 150-200, 200-300, 350-400	DNA	46-867	
62	G233	MYB	1-50, 50-75, 76-81, 82-100, 100-150, 150-200	protein		14-114
63	G920	WRKY	1-100, 30-48, 75-125, 150-200, 200-300, 350-400	DNA	114-1154	
64	G920	WRKY	1-50, 50-75, 76-81, 82-100, 100-150, 150-200	protein		152-211
65	G867	AP2	1-100, 30-48, 75-125, 150-200, 200-300, 350-400	DNA	64-1098	
66	G867	AP2	1-50, 50-75, 76-81, 82-100, 100-150, 150-200	protein		59-124
67	G659	MYB	1-100, 30-48, 75-125, 150-200, 200-300, 350-400	DNA	1-984	
68	G659	MYB	1-50, 50-75, 76-81, 82-100, 100-150, 150-200	protein		16-116
69	G620	CAAT	1-100, 30-48, 75-125, 150-200, 200-300, 350-400	DNA	40-666	
70	G620	CAAT	1-50, 50-75, 76-81, 82-100, 100-150, 150-200	protein		20-118
71	G596	AT-Hook	1-100, 30-48, 75-125, 150-200, 200-300, 350-400	DNA	168-1121	
72	G596	AT-Hook	1-50, 50-75, 76-81, 82-100, 100-150, 150-200	protein		89-96
73	G511	NAM	1-100, 30-48, 75-125, 150-200, 200-300, 350-400	DNA	31-738	
74	G511	NAM	1-50, 50-75, 76-81, 82-100, 100-150, 150-200	protein		8-159
75	G471	IAA/ARF	1-100, 30-48, 75-125, 150-200, 200-300, 350-400	DNA	115-2112	
76	G471	IAA/ARF	1-50, 50-75, 76-81, 82-100, 100-150, 150-200	protein		22-354
77	G385	HB	1-100, 30-48, 75-125, 150-200, 200-300, 350-400	DNA	37-2202	
78	G385	HB	1-50, 50-75, 76-81, 82-100, 100-150, 150-200	protein		60-123
79	G261	HS	1-100, 30-48, 75-125, 150-200, 200-300, 350-400	DNA	458-1663	
80	G261	HS	1-50, 50-75, 76-81, 82-100, 100-150, 150-200	protein		16-104
81	G25	AP2	1-100, 30-48, 75-125, 150-200, 200-300, 350-400	DNA	80-595	
82	G25	AP2	1-50, 50-75, 76-81, 82-100, 100-150, 150-200	protein		47-114
83	G610	BPF-1	1-100, 30-48, 75-125, 150-200, 200-300, 350-400	DNA	137-2059	
84	G610	BPF-1	1-50, 50-75, 76-81, 82-100, 100-150, 150-200	protein		577-609
85	G229	MYB	1-100, 30-48, 75-125, 150-200, 200-300, 350-400	DNA	41-1156	
86	G229	MYB	1-50, 50-75, 76-81, 82-100, 100-150, 150-200	protein		14-120
87	G221	MYB	1-100, 30-48, 75-125, 150-200, 200-300, 350-400	DNA	115-795	
88	G221	MYB	1-50, 50-75, 76-81, 82-100, 100-150, 150-200	protein		21-125
89	G186	WRKY	1-100, 30-48, 75-125, 150-200, 200-300, 350-400	DNA	100-1761	
90	G186	WRKY	1-50, 50-75, 76-81, 82-100, 100-150, 150-200	protein		312-369

Figure 1d

SEQ ID No	GID No.	Family	Fragments	DNA or protein	coding sequence	conserved domain
91	G562	bZIP	1-100, 30-48, 75-125, 150-200, 200-300, 350-400	DNA	137-1285	
92	G562	bZIP	1-50, 50-75, 76-81, 82-100, 100-150, 150-200	protein		253-315
93	G255	MYB	1-100, 30-48, 75-125, 150-200, 200-300, 350-400	DNA	30-839	
94	G255	MYB	1-50, 50-75, 76-81, 82-100, 100-150, 150-200	protein		14-115
95	G3	AP2	1-100, 30-48, 75-125, 150-200, 200-300, 350-400	DNA	16-477	
96	G3	AP2	1-50, 50-75, 76-81, 82-100, 100-150, 150-200	protein		11-95
97	G713	HB	1-100, 30-48, 75-125, 150-200, 200-300, 350-400	DNA	58-765	
98	G713	HB	1-50, 50-75, 76-81, 82-100, 100-150, 150-200	protein		23-86
99	G515	NAM	1-100, 30-48, 75-125, 150-200, 200-300, 350-400	DNA	154-1170	
100	G515	NAM	1-50, 50-75, 76-81, 82-100, 100-150, 150-200	protein		6-144
101	G390	HB	1-100, 30-48, 75-125, 150-200, 200-300, 350-400	DNA	1-2526	
102	G390	HB	1-50, 50-75, 76-81, 82-100, 100-150, 150-200	protein		18-81
103	G1034	bZIP	1-100, 30-48, 75-125, 150-200, 200-300, 350-400	DNA	214-1443	
104	G1034	bZIP	1-50, 50-75, 76-81, 82-100, 100-150, 150-200	protein		97-160
105	G1149	PAZ	1-100, 30-48, 75-125, 150-200, 200-300, 350-400	DNA	1-2910	
106	G1149	PAZ	1-50, 50-75, 76-81, 82-100, 100-150, 150-200	protein		870-880
107	G1334	CAAT	1-100, 30-48, 75-125, 150-200, 200-300, 350-400	DNA	76-885	
108	G1334	CAAT	1-50, 50-75, 76-81, 82-100, 100-150, 150-200	protein		18-190
109	G1650	HLH/MYC	1-100, 30-48, 75-125, 150-200, 200-300, 350-400	DNA	84-1199	
110	G1650	HLH/MYC	1-50, 50-75, 76-81, 82-100, 100-150, 150-200	protein		284-334
111	G241	MYB	1-100, 30-48, 75-125, 150-200, 200-300, 350-400	DNA		
112	G241	MYB	1-50, 50-75, 76-81, 82-100, 100-150, 150-200	protein		14-116
113	G348	GATA Zn	1-100, 30-48, 75-125, 150-200, 200-300, 350-400	DNA		
114	G171	MADS	1-100, 30-48, 75-125, 150-200, 200-300, 350-400	DNA		
115	G521	NAM	1-100, 30-48, 75-125, 150-200, 200-300, 350-400	DNA		
116	G1274	WRKY	1-100, 30-48, 75-125, 150-200, 200-300, 350-400	DNA		
117	G182	WRKY	1-100, 30-48, 75-125, 150-200, 200-300, 350-400	DNA		
118	G1290	AKR	1-100, 30-48, 75-125, 150-200, 200-300, 350-400	DNA		
119	G374	Z	1-100, 30-48, 75-125, 150-200, 200-300, 350-400	DNA		
120	G682	MYB	1-100, 30-48, 75-125, 150-200, 200-300, 350-400	DNA		

Figure 1e

SEQ ID No	GID No.	Family	Fragments	DNA or protein	coding sequence	conserved domain
121	G501	NAM	1-100, 30-48, 75-125, 150-200, 200-300, 350-400	DNA		

DECLARATION FOR UTILITY PATENT APPLICATION

As a below-named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name;

I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled:

Disease-induced polynucleotides

the specification of which is attached hereto.

I hereby state that I have reviewed and understand the contents of the above-identified specification, including the claims, as amended by any amendment referred to above.

I acknowledge the duty to disclose all information which is material to patentability as defined in Title 37, Code of Federal Regulations, § 1.56(a) which states in relevant part: "Each individual associated with the filing and prosecution of a patent application has a duty of candor and good faith in dealing with the Office, which includes a duty to disclose to the Office all information known to that individual to be material to patentability as defined in this section. The duty to disclose all information known to be material to patentability is deemed to be satisfied if all information known to be material to patentability of any claim issued in a patent was cited by the Office or submitted to the Office in the manner prescribed by §§ 1.97(b)-(d) and 1.98.

I hereby claim foreign priority benefits under Title 35 United States Code, § 119(a)-(d) or 365(a)-(b) of any foreign applications for patent or inventor's certificate as indicated below and have also identified below any foreign application for patent or inventor's certificate having a filing date before that of the application on which priority is claimed:

I hereby claim the benefit of priority under Title 35 United States Code, § 119(e) of any United States provisional application(s) listed below:

Provisional Serial No.:	Filing Date:
60/125,814	3/23/99

I hereby claim the benefit under Title 35 United States Code, § 120 of any United States applications listed below and, insofar as this is a continuation-in-part application filed under the conditions set forth in 35 United States Code, § 120, which discloses and claims subject matter in addition to the prior copending application(s) listed below, I acknowledge the duty to disclose to the United States Patent Office all information known to be material to patentability as defined in Title 37 Code of Federal Regulations, § 1.56 which became available between the filing date of the prior application and the national or PCT international filing date of this application:

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Title 18, United States Code,§1001 and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

Full name of first joint coinventor: Jacqueline Heard

Inventor's signature: Jacqueline Heard

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Post Office Address: Same as above.

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Inventor's signature: P. B

Date: 3-20-00

Citizenship: France

Residence: 921 Sunnybrae Blvd., San Mateo, CA 94402

Post Office Address: Same as above.

Full name of third joint coinventor: Jose Luis Riechmann

Inventor's signature:

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Citizenship: Spain.

Residence: 115 Moss Avenue, Apt. 308, Oakland, CA 94611

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Full name of fourth joint coinventor: James Keddie

Inventor's signature:

Date: 3-20-2000

Citizenship: U. K.

Residence: 54 McLellan Ave, San Mateo, CA 94403

Post Office Address: Same as above.

Full name of fifth joint coinventor: Omaira Pineda

Inventor's signature: Omaira Pineda

Date: 3/21/00

Citizenship: Colombia

Residence: 19563 Helen Place, Castro Valley, CA 94546

Post Office Address: Same as above.

Full name of sixth joint coinventor: Luc Adam

Inventor's signature: [signature]

Date: 03/20/00

Citizenship: Canada

Residence: 25800 Industrial Blvd. Apt. L403, Hayward, CA 94545

Post Office Address: Same as above.

Full name of seventh joint coinventor: Raymond Samaha

Inventor's signature: [signature]

Date: 3/20/00

Citizenship: U.S.

Residence: 2224 Albert Lane, Capitola, CA 95010

Post Office Address: Same as above.

Full name of eigth joint coinventor: James Zhang

Inventor's signature: [signature]

Date: 3/20/00

Citizenship: U. S.

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Post Office Address: Same as above.

Full name of ninth joint coinventor: Guo-Liang Yu

Inventor's signature:

Date: 03/20/2000

Citizenship: China

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Full name of tenth joint coinventor: Oliver Ratcliffe

Inventor's signature: Oliver J Ratcliffe

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Citizenship: U. K.

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Post Office Address: Same as above.

Full name of eleventh joint coinventor: Marsha Pilgrim

Inventor's signature: Marsha L. Pilgrim

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Post Office Address: Same as above.

Full name of twifth joint coinventor: Cai-Zhong Jiang

Inventor's signature: Caizhong Jiang

Date: 3/21/00

Citizenship: China

Residence: 34495 Heathrow Terrace, Fremont, CA 94555

Post Office Address: Same as above.

Full name of thirteenth joint coinventor: Lynne Reuber

Inventor's signature: T. Lynne Reuber

Date: 3/21/00

Citizenship: U.S.

Residence: 1115 S. Grant, San Mateo, CA 94402

Post Office Address: Same as above.

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

IN RE PATENT APPLICATION OF

Jacqueline Heard et al.

Examiner: Unknown

Group Art Unit: Unknown

Application No. Unassigned

Filing Date: Herewith

Title: **Disease-induced polynucleotides**

POWER OF ATTORNEY BY ASSIGNEE
TO EXCLUSION OF INVENTOR UNDER 37 C.F.R. § 3.71

Commissioner of Patents
and Trademarks
Washington, D.C. 20231

Sir:

The undersigned ASSIGNEE having an interest in the above-identified application for letters patent hereby appoints Karen J. Guerrero, Reg. No. 37,071 to prosecute this application and transact all business in the United States Patent and Trademark Office in connection therewith and hereby revokes all prior powers of attorney; said appointment to be to the exclusion of the inventors and the inventors' attorneys in accordance with the provisions of 3 7 C.F.R. § 3.7 1.

The following evidentiary documents establish a chain of title from the original owner to the Assignee:

X a copy of an Assignment attached hereto, which Assignment has been (or is herewith) forwarded to the Patent and Trademark Office for recording; or

- the Assignment recorded on at reel _, frames _ - _.

Pursuant to 37 C.F.R. § 3.73(b) the undersigned Assignee hereby states that evidentiary documents have been reviewed and hereby certifies that, to the best of ASSIGNEE's knowledge and belief, title is in the identified ASSIGNEE.

Direct all telephone calls to Karen J. Guerrero (510) 264-0280 ext. 125.

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ASSIGNEE: Mendel Biotechnology, Inc.

Name:

Name:
Guo-Liang Yu

Title:
Senior Vice-President, Research and Development

Date: 03/20/2000

SEQUENCE LISTING

<110> Heard, Jacqueline
Broun, Pierre
Riechmann, Jose-Luis
Keddie, James
Pineda, Omaira
Adam, Luc
Samaha, Raymond
Zhang, James
Yu, Guo-Liang
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Asp Gln Val Ser Gln Gly Gly Gly Ser Pro Lys Ser Asp Asp Ser Asp
65 70 75 80

Gln Glu Pro Leu Val Ile Lys Ser Ser Lys Lys Ser Met Pro Arg Trp
85 90 95

Ser Ser Lys Val Arg Ile Ala Pro Gly Ala Gly Val Asp Arg Thr Leu
100 105 110

Asp Asp Gly Phe Ser Trp Arg Lys Tyr Gly Gln Lys Asp Ile Leu Gly
115 120 125

Ala Lys Phe Pro Arg Gly Tyr Tyr Arg Cys Thr Tyr Arg Lys Ser Gln
130 135 140

Gly Cys Glu Ala Thr Lys Gln Val Gln Arg Ser Asp Glu Asn Gln Met
145 150 155 160

Leu Leu Glu Ile Ser Tyr Arg Gly Ile His Ser Cys Ser Gln Ala Ala
165 170 175

Asn Val Gly Thr Thr Met Pro Ile Gln Asn Leu Glu Pro Asn Gln Thr
180 185 190

Gln Glu His Gly Asn Leu Asp Met Val Lys Glu Ser Val Asp Asn Tyr
195 200 205

Asn His Gln Ala His Leu His His Asn Leu His Tyr Pro Leu Ser Ser
210 215 220

Thr Pro Asn Leu Glu Asn Asn Asn Ala Tyr Met Leu Gln Met Arg Asp
225 230 235 240

Gln Asn Ile Glu Tyr Phe Gly Ser Thr Ser Phe Ser Ser Asp Leu Gly
245 250 255

Thr Ser Ile Asn Tyr Asn Phe Pro Ala Ser Gly Ser Ala Ser His Ser
260 265 270

Ala Ser Asn Ser Pro Ser Thr Val Pro Leu Glu Ser Pro Phe Glu Ser
275 280 285

Tyr Asp Pro Asn His Pro Tyr Gly Gly Phe Gly Gly Phe Tyr Ser
290 295 300

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aagttatcgc agttagagca agaactcgaa aaggttaagc agcagggcca tttaggacca 600
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Lys Ser Asp Ile Asn Asp His Ser Pro Asn Thr Ala Thr Ser Ser Ile
35 40 45

Ile Gln Val Asp Pro Arg Ile Asp Asp His Asn Asn Asn Ile Lys Ile
50 55 60

Asn Tyr Asp Ser Ser His Asn Gln Ile Glu Ala Glu Gln Pro Ser Ser
65 70 75 80

Asn Asp Asn Gln Asp Asp Asp Gly Arg Ile His Asp Lys Met Lys Arg
85 90 95

Arg Leu Ala Gln Asn Arg Glu Ala Ala Arg Lys Ser Arg Leu Arg Lys
100 105 110

Lys Ala Tyr Val Gln Gln Leu Glu Glu Ser Arg Leu Lys Leu Ser Gln
115 120 125

Leu Glu Gln Glu Leu Glu Lys Val Lys Gln Gln Gly His Leu Gly Pro
130 135 140

Ser Gly Ser Ile Asn Thr Gly Ile Ala Ser Phe Glu Met Glu Tyr Ser
145 150 155 160

His Trp Leu Gln Glu Gln Ser Arg Arg Val Ser Glu Leu Arg Thr Ala
165 170 175

Leu Gln Ser His Ile Ser Asp Ile Glu Leu Lys Met Leu Val Glu Ser
180 185 190

Cys Leu Asn His Tyr Ala Asn Leu Phe Arg Met Lys Ser Asp Ala Ala
195 200 205

Lys Ala Asp Val Phe Tyr Leu Ile Ser Gly Met Trp Arg Thr Ser Thr
210 215 220

Glu Arg Phe Phe Gln Trp Ile Gly Gly Phe Arg Pro Ser Glu Leu Leu
225 230 235 240

Asn Val Val Met Pro Tyr Leu Gln Pro Leu Thr Asp Gln Gln Ile Leu
245 250 255

Glu Val Arg Asn Leu Gln Gln Ser Ser Gln Gln Ala Glu Asp Ala Leu
260 265 270

Ser Gln Gly Ile Asp Lys Leu Gln Gln Ser Leu Ala Glu Ser Ile Val
275 280 285

Ile Asp Ala Val Ile Glu Ser Thr His Tyr Pro Thr His Met Ala Ala
290 295 300

Ala Ile Glu Asn Leu Gln Ala Leu Glu Gly Phe Val Asn Gln Ala Asp
305 310 315 320

His Leu Arg Gln Gln Thr Leu Gln Gln Met Ala Lys Ile Leu Thr Thr
325 330 335

Arg Gln Ser Ala Arg Gly Leu Leu Ala Leu Gly Glu Tyr Leu His Arg
340 345 350

Leu Arg Ala Leu Ser Ser Leu Trp Ala Ala Arg Pro Gln Glu Pro Thr
355 360 365

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<220>
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ccaacactgc actcttcagt ccaagcacga agcagctctc tccgacaagg caaagttaga 300
gcatcaagtg cagtttctcc aagatgagct gaagagagca aggaatcagc ttgctctgtt 360
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<213> Arabidopsis thaliana

<220>
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Gln Asp Gln Val Arg Gln Leu Glu Lys Cys Phe Thr Met Asn Lys Lys
            20   25   30

Leu Glu Pro Asp Leu Lys Leu Gln Leu Ser Asn Gln Leu Gly Leu Pro
        35   40   45

Gln Arg Gln Val Ala Val Trp Phe Gln Asn Lys Arg Ala Arg Phe Lys
    50   55   60

Thr Gln Ser Leu Glu Val Gln His Cys Thr Leu Gln Ser Lys His Glu
65   70   75   80

Ala Ala Leu Ser Asp Lys Ala Lys Leu Glu His Gln Val Gln Phe Leu
                85   90   95

Gln Asp Glu Leu Lys Arg Ala Arg Asn Gln Leu Ala Leu Phe Thr Asn
            100   105   110

Gln Asp Ser Pro Val Asp Asn Ser Asn Leu Gly Ser Cys Asp Glu Asp
        115   120   125

His Asp Asp Gln Val Val Val Phe Asp Glu Leu Tyr Ala Cys Phe Val
    130   135   140

Ser Asn Gly His Gly Ser Ser Ser Thr Ser Trp Val
145   150   155

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<213> Arabidopsis thaliana

<220>
<223> G4

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aagtgaaagc ttcaaagaag agatcgaata agcgatccga tttcttcgat cttgacgatg 240
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<220>
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20 25 30

Lys Ala Ser Lys Lys Arg Ser Asn Lys Arg Ser Asp Phe Phe Asp Leu
35 40 45

Asp Asp Asp Phe Glu Ala Asp Phe Gln Gly Phe Lys Asp Asp Ser Ala
50 55 60

Phe Asp Cys Glu Asp Asp Asp Asp Val Phe Val Asn Val Lys Pro Phe
65 70 75 80

Val Phe Thr Ala Thr Thr Lys Pro Val Ala Ser Ala Phe Val Ser Thr
85 90 95

Val Gly Ser Ala Tyr Ala Lys Lys Thr Val Glu Ser Ala Glu Gln Ala
100 105 110

Glu Lys Ser Ser Lys Arg Lys Arg Lys Asn Gln Tyr Arg Gly Ile Arg
115 120 125

Gln Arg Pro Trp Gly Lys Trp Ala Ala Glu Ile Arg Asp Pro Arg Lys
130 135 140

Gly Ser Arg Glu Trp Leu Gly Thr Phe Asp Thr Ala Glu Glu Ala Ala
145 150 155 160

Arg Ala Tyr Asp Ala Ala Ala Arg Arg Ile Arg Gly Thr Lys Ala Lys
165 170 175

Val Asn Phe Pro Glu Glu Lys Asn Pro Ser Val Val Ser Gln Lys Arg
180 185 190

Pro Ser Ala Lys Thr Asn Asn Leu Gln Lys Ser Val Ala Lys Pro Asn
195 200 205

Lys Ser Val Thr Leu Val Gln Gln Pro Thr His Leu Ser Gln Gln Tyr
210 215 220

Cys Asn Asn Ser Phe Asp Asn Ser Phe Gly Asp Met Ser Phe Met Glu
225 230 235 240

Glu Lys Pro Gln Met Tyr Asn Asn Gln Phe Gly Leu Thr Asn Ser Phe
245 250 255

Asp Ala Gly Gly Asn Asn Gly Tyr Gln Tyr Phe Ser Ser Asp Gln Gly
260 265 270

Ser Asn Ser Phe Asp Cys Ser Glu Phe Gly Trp Ser Asp His Gly Pro
275 280 285

Lys Thr Pro Glu Ile Ser Ser Met Leu Val Asn Asn Asn Glu Ala Ser
290 295 300

Phe Val Glu Glu Thr Asn Ala Ala Lys Lys Leu Lys Pro Asn Ser Asp
305 310 315 320

Glu Ser Asp Asp Leu Met Ala Tyr Leu Asp Asn Ala Leu Trp Asp Thr
325 330 335

Pro Leu Glu Val Glu Ala Met Leu Gly Ala Asp Ala Gly Ala Val Thr
340 345 350

Gln Glu Glu Glu Asn Pro Val Glu Leu Trp Ser Leu Asp Glu Ile Asn
355 360 365

Phe Met Leu Glu Gly Asp Phe
370 375

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<213> Arabidopsis thaliana

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<223> G1035

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atgggatctt ccacaagtgg aaattgctcg tcggtttcaa ccactggttt agctaactcc 180

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<212> PRT
<213> Arabidopsis thaliana

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            20                  25                  30

Arg Gln Arg Asp Leu Ile Asp Glu Arg Lys Arg Lys Arg Lys Gln Ser
        35                  40                  45

Asn Arg Glu Ser Ala Arg Arg Ser Arg Met Arg Lys Gln Lys His Leu
    50                  55                  60

Asp Asp Leu Thr Ala Gln Val Thr His Leu Arg Lys Glu Asn Ala Gln
65                  70                  75                  80

Ile Val Ala Gly Ile Ala Val Thr Thr Gln His Tyr Val Thr Ile Glu
                85                  90                  95

Ala Glu Asn Asp Ile Leu Arg Ala Gln Val Leu Glu Leu Asn His Arg
            100                 105                 110

Leu Gln Ser Leu Asn Glu Ile Val Asp Phe Val Glu Ser Ser Ser Ser
        115                 120                 125

Gly Phe Gly Met Glu Thr Gly Gln Gly Leu Phe Asp Gly Gly Leu Phe
    130                 135                 140

Asp Gly Val Met Asn Pro Met Asn Leu Gly Phe Tyr Asn Gln Pro Ile
145                 150                 155                 160

Met Ala Ser Ala Ser Thr Ala Gly Asp Val Phe Asn Cys
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caagaacaat ccattcccca ggagctatta taagtgcaca gaagaaggat gcagagtgaa 360
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taaa 724

<210> 16
<211> 147
<212> PRT
<213> Arabidopsis thaliana

<220>
<223> G179

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Asp Pro Arg Leu Thr Glu Phe His Gly Val Asp Asn Ser Ala Gln Pro
20 25 30

Thr Thr Ser Ser Glu Glu Lys Pro Arg Ser Lys Lys Lys Lys Lys Glu
35 40 45

Arg Glu Ala Arg Tyr Ala Phe Gln Thr Arg Ser Gln Val Asp Ile Leu
50 55 60

Asp Asp Gly Tyr Arg Trp Arg Lys Tyr Gly Gln Lys Ala Val Lys Asn
65 70 75 80

Asn Pro Phe Pro Arg Ser Tyr Tyr Lys Cys Thr Glu Glu Gly Cys Arg
85 90 95

Val Lys Lys Gln Val Gln Arg Gln Trp Gly Asp Glu Gly Val Val Val
100 105 110

Thr Thr Tyr Gln Gly Val His Thr His Ala Val Asp Lys Pro Ser Asp
115 120 125

Asn Phe His His Ile Leu Thr Gln Met His Ile Phe Pro Pro Phe Cys
130 135 140

Leu Lys Glu
145

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<212> DNA
<213> Arabidopsis thaliana

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<223> G28

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<213> Arabidopsis thaliana

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Thr Ala Ser Ser Val Thr Gln Ser Cys Val Thr Gly Gln Ser Ile Lys
35 40 45

Pro Val Tyr Gly Arg Asn Pro Ser Phe Ser Lys Leu Tyr Pro Cys Phe
50 55 60

Thr Glu Ser Trp Gly Asp Leu Pro Leu Lys Glu Asn Asp Ser Glu Asp
65 70 75 80

Met Leu Val Tyr Gly Ile Leu Asn Asp Ala Phe His Gly Gly Trp Glu
85 90 95

Pro Ser Ser Ser Ser Ser Asp Glu Asp Arg Ser Ser Phe Pro Ser Val
100 105 110

Lys Ile Glu Thr Pro Glu Ser Phe Ala Ala Val Asp Ser Val Pro Val
115 120 125

Lys Lys Glu Lys Thr Ser Pro Val Ser Ala Ala Val Thr Ala Ala Lys
130 135 140

Gly Lys His Tyr Arg Gly Val Arg Gln Arg Pro Trp Gly Lys Phe Ala
145 150 155 160

Ala Glu Ile Arg Asp Pro Ala Lys Asn Gly Ala Arg Val Trp Leu Gly
165 170 175

Thr Phe Glu Thr Ala Glu Asp Ala Ala Leu Ala Tyr Asp Arg Ala Ala
180 185 190

Phe Arg Met Arg Gly Ser Arg Ala Leu Leu Asn Phe Pro Leu Arg Val
195 200 205

Asn Ser Gly Glu Pro Asp Pro Val Arg Ile Lys Ser Lys Arg Ser Ser
210 215 220

Phe Ser Ser Ser Asn Glu Asn Gly Ala Pro Lys Lys Arg Arg Thr Val
225 230 235 240

Ala Ala Gly Gly Gly Met Asp Lys Gly Leu Thr Val Lys Cys Glu Val
245 250 255

Val Glu Val Ala Arg Gly Asp Arg Leu Leu Val Leu
260 265

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<212> DNA
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<223> G1241

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ttaaggttag atcgcttttt gtttaaaaaa aaaaaaaaaa aa 822

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<211> 165
<212> PRT
<213> Arabidopsis thaliana

<220>
<223> G1241

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Gly Lys Gly Thr Val Arg Arg Lys Lys Lys Ala Val His Lys Thr Thr
20 25 30

Thr Thr Asp Asp Lys Arg Leu Gln Ser Thr Leu Lys Arg Val Gly Val
35 40 45

Asn Ser Ile Pro Ala Ile Glu Glu Val Asn Ile Phe Lys Asp Asp Val
50 55 60

Val Ile Gln Phe Ile Asn Pro Lys Val Gln Ala Ser Ile Ala Ala Asn
65 70 75 80

Thr Trp Val Val Ser Gly Thr Pro Gln Thr Lys Lys Leu Gln Asp Ile
85 90 95

Leu Pro Gln Ile Ile Ser Gln Leu Gly Pro Asp Asn Leu Asp Asn Leu
100 105 110

Arg Lys Leu Ala Glu Gln Phe Gln Lys Gln Ala Pro Gly Ala Gly Asp
115 120 125

Val Pro Ala Thr Ile Gln Glu Glu Asp Asp Asp Asp Asp Val Pro Asp
130 135 140

Leu Val Val Gly Glu Thr Phe Glu Thr Pro Ala Thr Glu Glu Ala Pro
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Lys Ala Ala Ala Ser
165

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<212> DNA
<213> Arabidopsis thaliana

<220>
<223> G19

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Ala Lys Gly Arg Lys Leu Thr Ala Glu Glu Leu Trp Ser Glu Leu Asp
            20                  25                  30

Ala Ser Ala Ala Asp Asp Phe Trp Gly Phe Tyr Ser Thr Ser Lys Leu
        35                  40                  45

His Pro Thr Asn Gln Val Asn Val Lys Glu Glu Ala Val Lys Lys Glu
    50                  55                  60

Gln Ala Thr Glu Pro Gly Lys Arg Arg Lys Arg Lys Asn Val Tyr Arg
65                  70                  75                  80

Gly Ile Arg Lys Arg Pro Trp Gly Lys Trp Ala Ala Glu Ile Arg Asp
                85                  90                  95

Pro Arg Lys Gly Val Arg Val Trp Leu Gly Thr Phe Asn Thr Ala Glu
            100                 105                 110

Glu Ala Ala Met Ala Tyr Asp Val Ala Ala Lys Gln Ile Arg Gly Asp
        115                 120                 125

Lys Ala Lys Leu Asn Phe Pro Asp Leu His His Pro Pro Pro Pro Asn
    130                 135                 140

Tyr Thr Pro Pro Pro Ser Ser Pro Arg Ser Thr Asp Gln Pro Pro Ala
145                 150                 155                 160
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Lys Lys Val Cys Val Val Ser Gln Ser Glu Ser Glu Leu Ser Gln Pro
165 170 175

Ser Phe Pro Val Glu Cys Ile Gly Phe Gly Asn Gly Asp Glu Phe Gln
180 185 190

Asn Leu Ser Tyr Gly Phe Glu Pro Asp Tyr Asp Leu Lys Gln Gln Ile
195 200 205

Ser Ser Leu Glu Ser Phe Leu Glu Leu Asp Gly Asn Thr Ala Glu Gln
210 215 220

Pro Ser Gln Leu Asp Glu Ser Val Ser Glu Val Asp Met Trp Met Leu
225 230 235 240

Asp Asp Val Ile Ala Ser Tyr Glu
245

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atttcatcct accgacgaag aactcatcgt ttactatctc cgaaaccaga ccatgtctaa 180
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acccgagaaa acagagtttg gagaaaatga gtggtatttc ttcagcccta gagaaagaaa 300
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<213> Arabidopsis thaliana

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<223> G503

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Ser Lys Pro Cys Pro Val Ser Ile Ile Pro Glu Val Asp Ile Tyr Lys
35 40 45

Phe Asp Pro Trp Gln Leu Pro Glu Lys Thr Glu Phe Gly Glu Asn Glu
50 55 60

Trp Tyr Phe Phe Ser Pro Arg Glu Arg Lys Tyr Pro Asn Gly Val Arg
65 70 75 80

Pro Asn Arg Ala Ala Val Ser Gly Tyr Trp Lys Ala Thr Gly Thr Asp
85 90 95

Lys Ala Ile His Ser Gly Ser Ser Asn Val Gly Val Lys Lys Ala Leu
100 105 110

Val Phe Tyr Lys Gly Arg Pro Pro Lys Gly Ile Lys Thr Asp Trp Ile
115 120 125

Met His Glu Tyr Arg Leu His Asp Ser Arg Lys Ala Ser Thr Lys Arg
130 135 140

Ser Gly Ser Met Arg Leu Asp Glu Trp Val Leu Cys Arg Ile Tyr Lys
145 150 155 160

Lys Arg Gly Ala Ser Lys Leu Leu Asn Glu Gln Glu Gly Phe Met Asp
165 170 175

Glu Val Leu Met Glu Asp Glu Thr Lys Val Val Ile Asn Glu Ala Glu
180 185 190

Arg Arg Asn Asp Glu Glu Ile Met Met Met Thr Ser Met Lys Leu Pro
195 200 205

Arg Thr Cys Ser Leu Ala His Leu Leu Glu Met Asp Tyr Met Gly Pro
210 215 220

Val Ser His Ile Asp Asn Phe Ser Gln Phe Asp His Leu His Gln Pro
225 230 235 240

Asp Ser Glu Ser Ser Trp Phe Gly Asp Leu Gln Phe Asn Gln Asp Glu
245 250 255

Ile Leu Asn His His Arg Gln Ala Met Phe Lys Phe
260 265

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<212> DNA
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<223> G263

<400> 25

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aaacagcaga gtttgctaaa gatcttcttc ctcaatactt caagcataat aatttctcaa 240
gcttcattcg tcagctcaac acttacggat ttcgtaaaac tgtaccggat aaatgggaat 300
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gcggaggagc agaggagggg gtaggtgaag gattgaaatt gtttggggtg tggttgaaag 780
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<212> PRT
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Ser Trp Asn Glu Glu Gly Thr Ala Phe Val Val Trp Lys Thr Ala Glu
35 40 45

Phe Ala Lys Asp Leu Leu Pro Gln Tyr Phe Lys His Asn Asn Phe Ser
50 55 60

Ser Phe Ile Arg Gln Leu Asn Thr Tyr Gly Phe Arg Lys Thr Val Pro
65 70 75 80

Asp Lys Trp Glu Phe Ala Asn Asp Tyr Phe Arg Arg Gly Gly Glu Asp
85 90 95

Leu Leu Thr Asp Ile Arg Arg Arg Lys Ser Val Ile Ala Ser Thr Ala
100 105 110

Gly Lys Cys Val Val Val Gly Ser Pro Ser Glu Ser Asn Ser Gly Gly
115 120 125

Gly Asp Asp His Gly Ser Ser Ser Thr Ser Ser Pro Gly Ser Ser Lys
130 135 140

Asn Pro Gly Ser Val Glu Asn Met Val Ala Asp Leu Ser Gly Glu Asn
145 150 155 160

Glu Lys Leu Lys Arg Glu Asn Asn Asn Leu Ser Ser Glu Leu Ala Ala
165 170 175

Ala Lys Lys Gln Arg Asp Glu Leu Val Thr Phe Leu Thr Gly His Leu
180 185 190

Lys Val Arg Pro Glu Gln Ile Asp Lys Met Ile Lys Gly Gly Lys Phe
195 200 205

Lys Pro Val Glu Ser Asp Glu Glu Ser Glu Cys Glu Gly Cys Asp Gly
210 215 220

Gly Gly Gly Ala Glu Glu Gly Val Gly Glu Gly Leu Lys Leu Phe Gly
225 230 235 240

Val Trp Leu Lys Gly Glu Arg Lys Lys Arg Asp Arg Asp Glu Lys Asn
245 250 255

Tyr Val Val Ser Gly Ser Arg Met Thr Glu Ile Lys Asn Val Asp Phe
260 265 270

His Ala Pro Leu Trp Lys Ser Ser Lys Val Cys Asn
275 280

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<220>
<223> "n" bases at various positions throughout the
sequence may be A, T, C, G, other or unknown

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tcagtactca tcctctttgg tcgatacttc attagatctc actattggcg ttactcgtat 180
gcgagttgaa gaagatccac cgacaagtgc tttggtggaa gaattaaacc gagttagtgc 240
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gaagcaactt atggaatatg ttaacaagag caacataacc gagagggatc aaatcagccc 360
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Ile Gly Val Thr Arg Met Arg Val Glu Glu Asp Pro Pro Thr Ser Ala
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Leu Val Glu Glu Leu Asn Arg Val Ser Ala Glu Asn Lys Lys Leu Ser
35 40 45

Glu Met Leu Thr Leu Met Cys Asp Asn Tyr Asn Val Leu Arg Lys Gln
50 55 60

Leu Met Glu Tyr Val Asn Lys Ser Asn Ile Thr Glu Arg Asp Gln Ile
65 70 75 80

Ser Pro Pro Lys Lys Arg Lys Ser Pro Ala Arg Glu Asp Ala Phe Ser
85 90 95

Cys Ala Val Ile Gly Gly Val Ser Glu Ser Ser Ser Thr Asp Gln Asp
100 105 110

Glu Tyr Leu Cys Lys Lys Gln Arg Glu Glu Thr Val Val Lys Glu Lys
115 120 125

Val Ser Arg Val Tyr Tyr Lys Thr Glu Ala Ser Asp Thr Thr Leu Val
130 135 140

Val Lys Asp Gly Tyr Gln Trp Arg Lys Tyr Gly Gln Lys Val Thr Arg
145 150 155 160

Asp Asn Pro Ser Pro Arg Ala Tyr Phe Lys Cys Ala Cys Ala Pro Ser
165 170 175

Cys Ser Val Lys Lys Lys Val Gln Arg Ser Val Glu Asp Gln Ser Val
180 185 190

Leu Val Ala Thr Tyr Glu Gly Glu His Asn His Pro Met Pro Ser Gln
195 200 205

Ile Asp Ser Asn Asn Gly Leu Asn Arg His Ile Ser His Gly Gly Ser
210 215 220

Ala Ser Thr Pro Val Ala Ala Asn Arg Arg Ser Ser Leu Thr Val Pro
225 230 235 240

Val Thr Thr Val Asp Met Ile Glu Ser Lys Lys Val Thr Ser Pro Thr
245 250 255

Ser Arg Ile Asp Phe Pro Gln Val Gln Lys Leu Leu Val Glu Gln Met
260 265 270

Ala Ser Ser Leu Thr Lys Asp Pro Asn Phe Thr Ala Ala Leu Ala Ala
275 280 285

Ala Val Thr Gly Lys Leu Tyr Gln Gln Asn His Thr Glu Lys
290 295 300

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<211> 748
<212> DNA
<213> Arabidopsis thaliana

<220>
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<213> Arabidopsis thaliana

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Asp Asp Asp Leu Val Ser Ala Val Ser Gly Met Asn Gln Ser Tyr Gly
35 40 45

Tyr Gln Thr Ser Asp Val Ala Gly Ala Leu Phe Ser Gly Ser Ser Ser
50 55 60

Cys Phe Ser His Pro Glu Ser Pro Ser Thr Lys Thr Tyr Val Ala Ala
65 70 75 80

Thr Ala Thr Ala Ser Ala Asp Asn Gln Asn Lys Lys Glu Lys Lys Lys
85 90 95

Ile Lys Gly Arg Val Ala Phe Lys Thr Arg Ser Glu Val Glu Val Leu
100 105 110

Asp Asp Gly Phe Lys Trp Arg Lys Tyr Gly Lys Lys Met Val Lys Asn
115 120 125

Ser Pro His Pro Arg Asn Tyr Tyr Lys Cys Ser Val Asp Gly Cys Pro
130 135 140

Val Lys Lys Arg Val Glu Arg Asp Arg Asp Asp Pro Ser Phe Val Ile
145 150 155 160

Thr Thr Tyr Glu Gly Ser His Asn His Ser Ser Met Asn
165 170

<210> 31
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<212> DNA
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<220>
<223> G242

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<212> PRT
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20 25 30

Ser Lys Ser Ile Pro Gly Arg Ser Gly Lys Ser Cys Arg Leu Arg Trp
35 40 45

Cys Asn Gln Leu Ser Pro Gln Val Glu His Arg Pro Phe Ser Ala Glu
50 55 60

Glu Asp Glu Thr Ile Ala Arg Ala His Ala Gln Phe Gly Asn Lys Trp
65 70 75 80

Ala Thr Ile Ala Arg Leu Leu Asn Gly Arg Thr Asp Asn Ala Val Lys
85 90 95

Asn His Trp Asn Ser Thr Leu Lys Arg Lys Cys Gly Gly Tyr Asp His
100 105 110

Arg Gly Tyr Asp Gly Ser Glu Asp His Arg Pro Val Lys Arg Ser Val
115 120 125

Ser Ala Gly Ser Pro Pro Val Val Thr Gly Leu Tyr Met Ser Pro Gly
130 135 140

Ser Pro Thr Gly Ser Asp Val Ser Asp Ser Ser Thr Ile Pro Ile Leu
145 150 155 160

Pro Ser Val Glu Leu Phe Lys Pro Val Pro Arg Pro Gly Ala Val Val
165 170 175

Leu Pro Leu Pro Ile Glu Thr Ser Ser Phe Ser Asp Asp Pro Pro Thr
180 185 190

Ser Leu Ser Leu Ser Leu Pro Gly Ala Asp Val Ser Glu Glu Ser Asn
195 200 205

Arg Ser His Glu Ser Thr Asn Ile Asn Asn Thr Thr Ser Ser Arg His
210 215 220

Asn His Asn Asn Thr Val Ser Phe Met Pro Phe Ser Gly Gly Phe Arg
225 230 235 240

Gly Ala Ile Glu Glu Met Gly Lys Ser Phe Pro Gly Asn Gly Gly Glu
245 250 255

Phe Met Ala Val Val Gln Glu Met Ile Lys Ala Glu Val Arg Ser Tyr
260 265 270

Met Thr Glu Met Gln Arg Asn Asn Gly Gly Gly Phe Val Gly Gly Phe
275 280 285

Ile Asp Asn Gly Met Ile Pro Met Ser Gln Ile Gly Val Gly Arg Ile
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Glu
305

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<212> DNA
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<223> G1006

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<212> PRT
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<220>
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            20   25   30

Asn Glu Ser Thr Pro Ser Ser Cys Phe Thr Glu Ser Trp Gly Gly Leu
        35   40   45

Pro Leu Lys Glu Asn Asp Ser Glu Asp Met Leu Val Tyr Gly Leu Leu
    50   55   60

Lys Asp Ala Phe His Phe Asp Thr Ser Ser Ser Asp Leu Ser Cys Leu
65   70   75   80

Phe Asp Phe Pro Ala Val Lys Val Glu Pro Thr Glu Asn Phe Thr Ala
85 90 95

Met Glu Glu Lys Pro Lys Lys Ala Ile Pro Val Thr Glu Thr Ala Val
100 105 110

Lys Ala Lys His Tyr Arg Gly Val Arg Gln Arg Pro Trp Gly Lys Phe
115 120 125

Ala Ala Glu Ile Arg Asp Pro Ala Lys Asn Gly Ala Arg Val Trp Leu
130 135 140

Gly Thr Phe Glu Thr Ala Glu Asp Ala Ala Leu Ala Tyr Asp Ile Ala
145 150 155 160

Ala Phe Arg Met Arg Gly Ser Arg Ala Leu Leu Asn Phe Pro Leu Arg
165 170 175

Val Asn Ser Gly Glu Pro Asp Pro Val Arg Ile Thr Ser Lys Arg Ser
180 185 190

Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Thr Ser Ser Ser Glu Asn
195 200 205

Gly Lys Leu Lys Arg Arg Arg Lys Ala Glu Asn Leu Thr Ser Glu Val
210 215 220

Val Gln Val Lys Cys Glu Val Gly Asp Glu Thr Arg Val Asp Glu Leu
225 230 235 240

Leu Val Ser

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<211> 725
<212> DNA
<213> Arabidopsis thaliana

<220>
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gccatttcca accaacggtc aaaacccgta cctcctctac ggattccaaa gccctacaaa 180
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gatgtggtta aggatcgaga atcatcagtt gcttgataag cttaacaatc tctctgagtc 420
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cattgaataa agcattttc cccgattcat atttatgaaa attttcttca agagtatgtt 600
tctttgtatg tatatgtgga gatgtatttc agggttttga taatatgacc ctttacgacg 660
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<211> 173
<212> PRT
<213> Arabidopsis thaliana

<220>
<223> G1049

<400> 36
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Ser Ile Leu Gln Ser Pro Tyr Pro Ser Asn Phe Pro Ile Ser Thr Pro
20 25 30

Phe Pro Thr Asn Gly Gln Asn Pro Tyr Leu Leu Tyr Gly Phe Gln Ser
35 40 45

Pro Thr Asn Asn Pro Gln Ser Met Ser Leu Ser Ser Asn Asn Ser Thr
50 55 60

Ser Asp Glu Ala Glu Glu Gln Gln Thr Asn Asn Asn Ile Ile Asn Glu
65 70 75 80

Arg Lys Gln Arg Arg Met Ile Ser Asn Arg Glu Ser Ala Arg Arg Ser
85 90 95

Arg Met Arg Lys Gln Arg His Leu Asp Glu Leu Trp Ser Gln Val Met
100 105 110

Trp Leu Arg Ile Glu Asn His Gln Leu Leu Asp Lys Leu Asn Asn Leu
115 120 125

Ser Glu Ser His Asp Lys Val Leu Gln Glu Asn Ala Gln Leu Lys Glu
130 135 140

Glu Thr Phe Glu Leu Lys Gln Val Ile Ser Asp Met Gln Ile Gln Ser
145 150 155 160

Pro Phe Ser Cys Phe Arg Asp Asp Ile Ile Pro Ile Glu
165 170

<210> 37
<211> 1409
<212> DNA
<213> Arabidopsis thaliana

<220>
<223> G502

<400> 37
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cctccattca tagtaacaat aatattaaga aagagggtaa actatgtcag aattattaca 240
gttgcctcca ggtttccgat ttcaccctac cgatgaagag cttgtcatgc actatctctg 300
ccgcaaatgt gcctctcagt ccatcgccgt tccgatcatc gctgagatcg atctctacaa 360

atacgatcca tgggagcttc ctggtttagc cttgtatggt gagaaggaat ggtacttctt 420
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gcacgagtac cgtctcgccg acgttgaccg gtccgttcgc aagaagaaga atagtctcag 660
gctggatgat tgggttctct gccggattta caacaaaaaa ggagctaccg agaggcgggg 720
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<210> 38
<211> 319
<212> PRT
<213> Arabidopsis thaliana

<220>
<223> G502

<400> 38
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Asp Glu Glu Leu Val Met His Tyr Leu Cys Arg Lys Cys Ala Ser Gln
20 25 30

Ser Ile Ala Val Pro Ile Ile Ala Glu Ile Asp Leu Tyr Lys Tyr Asp
35 40 45

Pro Trp Glu Leu Pro Gly Leu Ala Leu Tyr Gly Glu Lys Glu Trp Tyr
50 55 60

Phe Phe Ser Pro Arg Asp Arg Lys Tyr Pro Asn Gly Ser Arg Pro Asn
65 70 75 80

Arg Ser Ala Gly Ser Gly Tyr Trp Lys Ala Thr Gly Ala Asp Lys Pro
85 90 95

Ile Gly Leu Pro Lys Pro Val Gly Ile Lys Lys Ala Leu Val Phe Tyr
100 105 110

Ala Gly Lys Ala Pro Lys Gly Glu Lys Thr Asn Trp Ile Met His Glu
115 120 125

Tyr Arg Leu Ala Asp Val Asp Arg Ser Val Arg Lys Lys Lys Asn Ser
130 135 140

Leu Arg Leu Asp Asp Trp Val Leu Cys Arg Ile Tyr Asn Lys Lys Gly
145 150 155 160

Ala Thr Glu Arg Arg Gly Pro Pro Pro Pro Val Val Tyr Gly Asp Glu
165 170 175

Ile Met Glu Glu Lys Pro Lys Val Thr Glu Met Val Met Pro Pro Pro
180 185 190

Pro Gln Gln Thr Ser Glu Phe Ala Tyr Phe Asp Thr Ser Asp Ser Val
195 200 205

Pro Lys Leu His Thr Thr Asp Ser Ser Cys Ser Glu Gln Val Val Ser
210 215 220

Pro Glu Phe Thr Ser Glu Val Gln Ser Glu Pro Lys Trp Lys Asp Trp
225 230 235 240

Ser Ala Val Ser Asn Asp Asn Asn Asn Thr Leu Asp Phe Gly Phe Asn
245 250 255

Tyr Ile Asp Ala Thr Val Asp Asn Ala Phe Gly Gly Gly Gly Ser Ser
260 265 270

Asn Gln Met Phe Pro Leu Gln Asp Met Phe Met Tyr Met Gln Lys Pro
275 280 285

Tyr Lys Gly Ile Pro Phe Leu Pro Pro Lys Arg Asn Ala Lys Arg Pro
290 295 300

Ser Phe Leu Arg Leu Trp Gln His Glu Thr Val Leu Tyr Gly Gln
305 310 315

<210> 39
<211> 1347
<212> DNA
<213> Arabidopsis thaliana

<220>
<223> G239

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ggcgatgctc gttggaacca catcgctcgt tcctctgggc taaagcgaac tggtaagagt 180
tgtagattaa gatggcttaa ttacttacgt ccagatgtta gaagaggcaa catcactctc 240
gaagaacaat ttatgatcct caaactccat tctctttggg gcaataggtg gtcgaagatt 300
gcgcaatatc taccgggaag aacagataat gaaataaaga attattggag aactcgagtc 360
caaaagcaag ccaaacacct aagatgcgat gttaacagta atcttttcaa ggagactatg 420
agaaatgttt ggatgccgag attagtggaa cgaatcaacg cccaatcatt acccaccacg 480
tgtgaacaag tggagtcaat gatcaccgac ccaagtcaac cagttaacga accgagtccg 540
gtcgagccgg gtttcgttca attcagccag aatcatcatc agcaattcgt accggctacg 600
gaattgtcag caacgtcttc gaattctccg gctgagacgt tttcggacgt tcgaggtggg 660
gtggtgaacg ggtcaggtta tgatccgtcg ggtcaaacgg gtttcggaga gttcaacgat 720
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gaatgctgca tggttgatcc taagaaa 1347

<210> 40
<211> 273
<212> PRT
<213> Arabidopsis thaliana

<220>
<223> G239

<400> 40
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Asp Ser Asp Val Arg Lys Gly Pro Trp Thr Glu Glu Glu Asp Ala Ile
20 25 30

Leu Val Asn Phe Val Ser Ile His Gly Asp Ala Arg Trp Asn His Ile
35 40 45

Ala Arg Ser Ser Gly Leu Lys Arg Thr Gly Lys Ser Cys Arg Leu Arg
50 55 60

Trp Leu Asn Tyr Leu Arg Pro Asp Val Arg Arg Gly Asn Ile Thr Leu
65 70 75 80

Glu Glu Gln Phe Met Ile Leu Lys Leu His Ser Leu Trp Gly Asn Arg
85 90 95

Trp Ser Lys Ile Ala Gln Tyr Leu Pro Gly Arg Thr Asp Asn Glu Ile
100 105 110

Lys Asn Tyr Trp Arg Thr Arg Val Gln Lys Gln Ala Lys His Leu Arg
115 120 125

Cys Asp Val Asn Ser Asn Leu Phe Lys Glu Thr Met Arg Asn Val Trp
130 135 140

Met Pro Arg Leu Val Glu Arg Ile Asn Ala Gln Ser Leu Pro Thr Thr
145 150 155 160

Cys Glu Gln Val Glu Ser Met Ile Thr Asp Pro Ser Gln Pro Val Asn
165 170 175

Glu Pro Ser Pro Val Glu Pro Gly Phe Val Gln Phe Ser Gln Asn His
180 185 190

His Gln Gln Phe Val Pro Ala Thr Glu Leu Ser Ala Thr Ser Ser Asn
195 200 205

Ser Pro Ala Glu Thr Phe Ser Asp Val Arg Gly Gly Val Val Asn Gly
210 215 220

Ser Gly Tyr Asp Pro Ser Gly Gln Thr Gly Phe Gly Glu Phe Asn Asp
225 230 235 240

Trp Gly Cys Val Gly Gly Asp Asn Met Trp Thr Asp Glu Glu Ser Phe
245 250 255

Trp Phe Leu Gln Asp Gln Phe Cys Pro Asp Thr Thr Ser Tyr Ser Tyr
260 265 270

Asn

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<212> DNA
<213> Arabidopsis thaliana

<220>
<223> G555

<400> 41
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cgagcaactt ttgtttgggg ttaagctcaa agaatccgtt cttttcagtc tttactccat 180
ctagggtacc acgattggat cggtttttat ctgatgattt agtaacagag attttgaaga 240
aaaagaaaaa tgggagatac tagtccaaga acatcagtct caacagatgg agacactgat 300
cataataacc taatgttcga tgaagggcat ttgggtatcg gtgcttctga ttctagtgac 360
cgttcaaaga gtaaaatgga tcaaaagacg cttcgtaggc tcgctcaaaa ccgtgaggct 420
gcaaggaaaa gcagattgag gaagaaagca tatgttcagc agctagagaa cagtcgattg 480
aagctaacac aacttgagca ggagctacaa agagcacggc aacagggtgt ctttatctca 540
agctctggag accaagccca ttctaccgct ggagatgggg caatggcatt tgatgtagaa 600
tacagacgat ggcaggaaga taaaaacaga cagatgaagg agctgagttc tgctatagat 660
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gagctttaca ggataaaagg caacgcagct aagagtgatg tcttccattt attatcaggg 780
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cgtgctctta gctctctatg gcttgccaga ccaagagagt gaaccatgac tctattatac 1260
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<210> 42
<211> 330
<212> PRT
<213> Arabidopsis thaliana

<220>
<223> G555

<400> 42

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Asp His Asn Asn Leu Met Phe Asp Glu Gly His Leu Gly Ile Gly Ala
            20   25   30

Ser Asp Ser Ser Asp Arg Ser Lys Ser Lys Met Asp Gln Lys Thr Leu
        35   40   45

Arg Arg Leu Ala Gln Asn Arg Glu Ala Ala Arg Lys Ser Arg Leu Arg
    50   55   60

Lys Lys Ala Tyr Val Gln Gln Leu Glu Asn Ser Arg Leu Lys Leu Thr
65   70   75   80

Gln Leu Glu Gln Glu Leu Gln Arg Ala Arg Gln Gln Gly Val Phe Ile
                85   90   95

Ser Ser Ser Gly Asp Gln Ala His Ser Thr Ala Gly Asp Gly Ala Met
            100   105   110

Ala Phe Asp Val Glu Tyr Arg Arg Trp Gln Glu Asp Lys Asn Arg Gln
        115   120   125

Met Lys Glu Leu Ser Ser Ala Ile Asp Ser His Ala Thr Asp Ser Glu
    130   135   140

Leu Arg Ile Ile Val Asp Gly Val Ile Ala His Tyr Glu Glu Leu Tyr
145   150   155   160

Arg Ile Lys Gly Asn Ala Ala Lys Ser Asp Val Phe His Leu Leu Ser
                165   170   175

Gly Met Trp Lys Thr Pro Ala Glu Arg Cys Phe Leu Trp Leu Gly Gly
            180   185   190

Phe Arg Ser Ser Glu Leu Leu Lys Leu Ile Ala Cys Gln Leu Glu Pro
        195   200   205

Leu Thr Glu Gln Gln Ser Leu Asp Ile Asn Asn Leu Gln Gln Ser Thr
    210   215   220

Gln Gln Ala Glu Asp Ala Leu Ser Gln Gly Met Asp Asn Leu Gln Gln
225   230   235   240

Ser Leu Ala Asp Thr Leu Ser Ser Gly Thr Leu Gly Ser Ser Ser Ser
                245   250   255

Gly Asn Val Ala Ser Tyr Met Gly Gln Met Ala Met Ala Met Gly Lys
            260   265   270

Leu Gly Thr Leu Glu Gly Phe Ile Arg Gln Ala Asp Asn Leu Arg Leu
        275   280   285

Gln Thr Tyr Gln Gln Met Val Arg Leu Leu Thr Thr Arg Gln Ser Ala
    290   295   300

Arg Ala Leu Leu Ala Val His Asn Tyr Thr Leu Arg Leu Arg Ala Leu
305 310 315 320

Ser Ser Leu Trp Leu Ala Arg Pro Arg Glu
325 330

<210> 43
<211> 817
<212> DNA
<213> Arabidopsis thaliana

<220>
<223> G352

<400> 43
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cgctcggcct cttctccggt atcgtgaaga aatggagcct gagaatctcg agcaatgggc 180
taaaagaaaa cgaacaaaac gtcaacgttt tgatcacggt catcagaatc aagaaacgaa 240
caagaacctt ccttctgaag aagagtatct cgctctttgt ctcctcatgc tcgctcgtgg 300
ctccgccgta caatctcctc ctcttcctcc tctaccgtca cgtgcgtcac cgtccgatca 360
ccgagattac aagtgtacgg tctgtgggaa gtccttttcg tcataccaag ccttaggtgg 420
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cggtaacgga agtagcagca acagcgtaga actcgtcgct ggtagtgacg tcagcgatgt 720
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cttaccggct gatcaagtct cagtgacgac ttcttaa 817

<210> 44
<211> 245
<212> PRT
<213> Arabidopsis thaliana

<220>
<223> G352

<400> 44
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Pro Leu Leu Arg Tyr Arg Glu Glu Met Glu Pro Glu Asn Leu Glu Gln
20 25 30

Trp Ala Lys Arg Lys Arg Thr Lys Arg Gln Arg Phe Asp His Gly His
35 40 45

Gln Asn Gln Glu Thr Asn Lys Asn Leu Pro Ser Glu Glu Glu Tyr Leu
50 55 60

Ala Leu Cys Leu Leu Met Leu Ala Arg Gly Ser Ala Val Gln Ser Pro
65 70 75 80

Pro Leu Pro Pro Leu Pro Ser Arg Ala Ser Pro Ser Asp His Arg Asp
85 90 95

Tyr Lys Cys Thr Val Cys Gly Lys Ser Phe Ser Ser Tyr Gln Ala Leu
100 105 110

Gly Gly His Lys Thr Ser His Arg Lys Pro Thr Asn Thr Ser Ile Thr
115 120 125

Ser Gly Asn Gln Glu Leu Ser Asn Asn Ser His Ser Asn Ser Gly Ser
130 135 140

Val Val Ile Asn Val Thr Val Asn Thr Gly Asn Gly Val Ser Gln Ser
145 150 155 160

Gly Lys Ile His Thr Cys Ser Ile Cys Phe Lys Ser Phe Ala Ser Gly
165 170 175

Gln Ala Leu Gly Gly His Lys Arg Cys His Tyr Asp Gly Gly Asn Asn
180 185 190

Gly Asn Gly Asn Gly Ser Ser Ser Asn Ser Val Glu Leu Val Ala Gly
195 200 205

Ser Asp Val Ser Asp Val Asp Asn Glu Arg Trp Ser Glu Glu Ser Ala
210 215 220

Ile Gly Gly His Arg Gly Phe Asp Leu Asn Leu Pro Ala Asp Gln Val
225 230 235 240

Ser Val Thr Thr Ser
245

<210> 45
<211> 1001
<212> DNA
<213> Arabidopsis thaliana

<220>
<223> G1352

<400> 45
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agaatcgaaa cgaaagaaga tttgatgaac gacgccgttt tcattgagcc gtggcttaaa 180
cgcaaacgct ccaaacgtca gcgttctcac agcccttctt cgtcttcttc ctcaccgcct 240
cgatctcgac ccaaatccca gaatcaagat cttacggaag aagagtatct cgctctttgt 300
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<210> 46
<211> 273
<212> PRT
<213> Arabidopsis thaliana

<220>
<223> G1352

<400> 46
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Glu Thr Lys Glu Asp Leu Met Asn Asp Ala Val Phe Ile Glu Pro Trp
            20   25   30

Leu Lys Arg Lys Arg Ser Lys Arg Gln Arg Ser His Ser Pro Ser Ser
        35   40   45

Ser Ser Ser Ser Pro Pro Arg Ser Arg Pro Lys Ser Gln Asn Gln Asp
    50   55   60

Leu Thr Glu Glu Glu Tyr Leu Ala Leu Cys Leu Leu Met Leu Ala Lys
65   70   75   80

Asp Gln Pro Ser Gln Thr Arg Phe His Gln Gln Ser Gln Ser Leu Thr
                85   90   95

Pro Pro Pro Glu Ser Lys Asn Leu Pro Tyr Lys Cys Asn Val Cys Glu
            100   105   110

Lys Ala Phe Pro Ser Tyr Gln Ala Leu Gly Gly His Lys Ala Ser His
        115   120   125

Arg Ile Lys Pro Pro Thr Val Ile Ser Thr Thr Ala Asp Asp Ser Thr
    130   135   140

Ala Pro Thr Ile Ser Ile Val Ala Gly Glu Lys His Pro Ile Ala Ala
145   150   155   160

Ser Gly Lys Ile His Glu Cys Ser Ile Cys His Lys Val Phe Pro Thr
                165   170   175

Gly Gln Ala Leu Gly Gly His Lys Arg Cys His Tyr Glu Gly Asn Leu
            180   185   190

Gly Gly Gly Gly Gly Gly Gly Ser Lys Ser Ile Ser His Ser Gly Ser
        195   200   205

Val Ser Ser Thr Val Ser Glu Glu Arg Ser His Arg Gly Phe Ile Asp
    210   215   220

Leu Asn Leu Pro Ala Leu Pro Glu Leu Ser Leu His His Asn Pro Ile
225   230   235   240

Val Asp Glu Glu Ile Leu Ser Pro Leu Thr Gly Lys Lys Pro Leu Leu
                245   250   255

Leu Thr Asp His Asp Gln Val Ile Lys Lys Glu Asp Leu Ser Leu Lys
260 265 270

Ile

<210> 47
<211> 2663
<212> DNA
<213> Arabidopsis thaliana

<220>
<223> G1089

<400> 47
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gctctttccg attactctca cggcgagttt ttagtctcta atcactcgtc ttcctccgca 240
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tccaccgctc cggtttctaa ttcaaccgct tcttcttcct ccgctgcggt tcctcagccg 360
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attgaagaag atggagccct agataacgat gatgatgacg atgatgatga tgatgactct 540
gaaatggaga atcgtgatcg tttgattagg aaatcgagaa gccgtggagg tagtactaga 600
ggaaatagga cgacgattga agatcatcat cttcaggagg agaaagctcc gccacctccc 660
cctttggcga attcgcggcc aattccgccg ccacgtcagc atcagcatca acatcagcaa 720
cagcaacaac aacctttcta cgattacttc ttccctaatg ttgagaatat gcctggaact 780
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ccacattcac cagtcgttac tgaggatgac gaagatgagg aggaggaaga ggaggaagag 900
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35 40 45

Gly Ala Ala Leu Ser Asp Tyr Ser His Gly Glu Phe Leu Val Ser Asn
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His Ser Ser Ser Ser Ala Ala Ala Ala Ile Ala Ser Thr Ser Ser Leu
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Pro Thr Ala Ile Ser Pro Pro Leu Pro Ser Ser Thr Ala Pro Val Ser
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Asn Ser Thr Ala Ser Ser Ser Ser Ala Ala Val Pro Gln Pro Ile Pro
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Asp Thr Leu Pro Pro Pro Pro Pro Pro Pro Pro Leu Pro Leu Gln Arg
115 120 125

Ala Ala Thr Met Pro Glu Met Asn Gly Arg Ser Gly Gly Gly His Ala
130 135 140

Gly Ser Gly Leu Asn Gly Ile Glu Glu Asp Gly Ala Leu Asp Asn Asp
145 150 155 160

Asp Asp Asp Asp Asp Asp Asp Asp Asp Ser Glu Met Glu Asn Arg Asp
165 170 175

Arg Leu Ile Arg Lys Ser Arg Ser Arg Gly Gly Ser Thr Arg Gly Asn
180 185 190

Arg Thr Thr Ile Glu Asp His His Leu Gln Glu Glu Lys Ala Pro Pro
195 200 205

Pro Pro Pro Leu Ala Asn Ser Arg Pro Ile Pro Pro Pro Arg Gln His
210 215 220

Gln His Gln His Gln Gln Gln Gln Gln Gln Pro Phe Tyr Asp Tyr Phe
225 230 235 240

Phe Pro Asn Val Glu Asn Met Pro Gly Thr Thr Leu Glu Asp Thr Pro
245 250 255

Pro Gln Pro Gln Pro Gln Pro Thr Arg Pro Val Pro Pro Gln Pro His
260 265 270

Ser Pro Val Val Thr Glu Asp Asp Glu Asp Glu Glu Glu Glu Glu Glu
275 280 285

Glu Glu Glu Glu Glu Glu Glu Thr Val Ile Glu Arg Lys Pro Leu Val
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Glu Glu Arg Pro Lys Arg Val Glu Glu Val Thr Ile Glu Leu Glu Lys
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Val Thr Asn Leu Arg Gly Met Lys Lys Ser Lys Gly Ile Gly Ile Pro
325 330 335

Gly Glu Arg Arg Gly Met Arg Met Pro Val Thr Ala Thr His Leu Ala
340 345 350

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355 360 365

Ala His Asp Val Ser Lys Met Leu Glu Ala Thr Arg Leu His Tyr His
370 375 380

Ser Asn Phe Ala Asp Asn Arg Gly His Ile Asp His Ser Ala Arg Val
385 390 395 400

Met Arg Val Ile Thr Trp Asn Arg Ser Phe Arg Gly Ile Pro Asn Ala
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Asp Asp Gly Lys Asp Asp Val Asp Leu Glu Glu Asn Glu Thr His Ala
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Thr Val Leu Asp Lys Leu Leu Ala Trp Glu Lys Lys Leu Tyr Asp Glu
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Val Lys Ala Gly Glu Leu Met Lys Ile Glu Tyr Gln Lys Lys Val Ala
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Glu Gln Leu Tyr Leu Lys Leu Val His Leu Val Glu Ala Met Gly Lys
515 520 525

Met Trp Glu Met Met Gln Ile His His Gln Arg Gln Ala Glu Ile Ser
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565 570 575

Trp His Thr Gln Phe Cys Arg Met Ile Asp His Gln Lys Glu Tyr Ile
580 585 590

Lys Ala Leu Gly Gly Trp Leu Lys Leu Asn Leu Ile Pro Ile Glu Ser
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Thr Leu Lys Glu Lys Val Ser Ser Pro Pro Arg Val Pro Asn Pro Ala
610 615 620

Ile Gln Lys Leu Leu His Ala Trp Tyr Asp Arg Leu Asp Lys Ile Pro
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Asp Glu Met Ala Lys Ser Ala Ile Ile Asn Phe Ala Ala Val Val Ser
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Thr Ile Met Gln Gln Gln Glu Asp Glu Ile Ser Leu Arg Asn Lys Cys
660 665 670

Glu Glu Thr Arg Lys Glu Leu Gly Arg Lys Ile Arg Gln Phe Glu Asp
675 680 685

Trp Tyr His Lys Tyr Ile Gln Lys Arg Gly Pro Glu Gly Met Asn Pro
690 695 700

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Asn Val Glu Gln Ile Lys Lys Arg Leu Glu Glu Glu Glu Glu Ala Tyr
725 730 735

His Arg Gln Ser His Gln Val Arg Glu Lys Ser Leu Ala Ser Leu Arg
740 745 750

Thr Arg Leu Pro Glu Leu Phe Gln Ala Met Ser Glu Val Ala Tyr Ser
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770 775 780

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Asn Gln Ser Ser Ser Thr Thr Leu Glu Val Asp Ala Arg Pro Glu Ala
50 55 60

Asp Asp Asn Asn Arg Val Asn Tyr Thr Ser Val Tyr Asn Asn Ser Leu
65 70 75 80

Glu Ala Glu Pro Ser Ser Asn Asn Asp Gln Asp Glu Asp Arg Ile Asn
85 90 95

Asp Lys Met Lys Arg Arg Leu Ala Gln Asn Arg Glu Ala Ala Arg Lys
100 105 110

Ser Arg Leu Arg Lys Lys Ala His Val Gln Gln Leu Glu Glu Ser Arg
115 120 125

Leu Lys Leu Ser Gln Leu Glu Gln Glu Leu Val Arg Ala Arg Gln Gln
130 135 140

Gly Leu Cys Val Arg Asn Ser Ser Asp Thr Ser Tyr Leu Gly Pro Ala
145 150 155 160

Gly Asn Met Asn Ser Gly Ile Ala Ala Phe Glu Met Glu Tyr Thr His
165 170 175

Trp Leu Glu Glu Gln Asn Arg Arg Val Ser Glu Ile Arg Thr Ala Leu
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Gln Ala His Ile Gly Asp Ile Glu Leu Lys Met Leu Val Asp Ser Cys
195 200 205

Leu Asn His Tyr Ala Asn Leu Phe Arg Met Lys Ala Asp Ala Ala Lys
210 215 220

Ala Asp Val Phe Phe Leu Met Ser Gly Met Trp Arg Thr Ser Thr Glu
225 230 235 240

Arg Phe Phe Gln Trp Ile Gly Gly Phe Arg Pro Ser Glu Leu Leu Asn
245 250 255

Val Val Met Pro Tyr Val Glu Pro Leu Thr Asp Gln Gln Leu Leu Glu
260 265 270

Val Arg Asn Leu Gln Gln Ser Ser Gln Gln Ala Glu Glu Ala Leu Ser
275 280 285

Gln Gly Leu Asp Lys Leu Gln Gln Gly Leu Val Glu Ser Ile Ala Ile
290 295 300

Gln Ile Lys Val Val Glu Ser Val Asn His Gly Ala Pro Met Ala Ser
305 310 315 320

Ala Met Glu Asn Leu Gln Ala Leu Glu Ser Phe Val Asn Gln Ala Asp
325 330 335

His Leu Arg Gln Gln Thr Leu Gln Gln Met Ser Lys Ile Leu Thr Thr
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Ala Ser Leu Ile Ile Gly Ile Ile Tyr Ser Val Ile Val Met Lys Leu
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Leu Ala Phe Val Phe Leu Arg Ser Trp Thr Lys Leu Leu Thr Lys Ala
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Gly Ile Val Thr Lys Pro Phe Thr Lys Gln Glu Asn Thr Val Val Gln
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Thr Cys Ala Val Ala Cys Tyr Ser Ile Ala Val Gly Gly Gly Phe Gly
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Ser Tyr Leu Leu Gly Leu Asn Arg Ile Thr Tyr Glu Gln Ser Gly Gly
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Thr His Thr Asp Gly Asn Tyr Pro Glu Gly Thr Lys Glu Pro Gly Ile
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Gly Trp Met Thr Ala Phe Leu Phe Phe Thr Cys Phe Val Gly Leu Leu
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Ala Leu Val Pro Leu Arg Lys Ile Met Ile Ile Asp Tyr Lys Leu Thr
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Tyr Pro Ser Gly Thr Ala Thr Ala Val Leu Ile Asn Gly Phe His Thr
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Pro Lys Gly Asn Lys Met Ala Lys Lys Gln Val Phe Gly Phe Val Lys
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Tyr Phe Ser Phe Ser Phe Ile Trp Ala Phe Phe Gln Trp Phe Phe Ser
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Gly Gly Thr Glu Cys Gly Phe Ile Gln Phe Pro Thr Phe Gly Leu Glu
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Ala Leu Lys Asn Thr Phe Tyr Phe Asp Phe Ser Met Thr Tyr Val Gly
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Ala Gly Met Ile Cys Pro His Ile Val Asn Ile Ser Leu Leu Phe Gly
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Ala Val Leu Ser Trp Gly Ile Met Trp Pro Leu Ile Lys Gly Leu Lys
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Leu Tyr Gln Phe Ile Lys Ile Leu Phe Lys Thr Gly Ile Asn Met Tyr
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Val Lys Leu Asn Asn Arg Asn Ser Gly Lys Ser Asn Ser Glu Lys Asp
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Lys Gln Ser Ile Ala Asp Leu Lys Arg Asp Glu Ile Phe Val Arg Asp
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Ser Ile Pro Leu Trp Val Ala Ala Val Gly Asn Ala Ala Phe Ser Val
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Val Ser Ile Ile Ala Ile Pro Ile Met Phe Pro Glu Leu Lys Trp Tyr
                405                 410                 415

Phe Ile Val Val Ala Tyr Met Leu Ala Pro Ser Leu Gly Phe Ser Asn
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Ala Tyr Gly Ala Gly Leu Thr Asp Met Asn Met Ala Tyr Asn Tyr Gly
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Lys Val Ala Leu Phe Ile Leu Ala Ala Met Ala Gly Lys Gln Asn Gly
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Ile Ser Ser Asp Leu Met His Asp Phe Lys Thr Gly His Leu Thr Leu
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Thr Ser Pro Arg Ser Met Leu Val Ser Gln Ala Ile Gly Thr Ala Ile
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Gly Cys Val Val Ala Pro Leu Thr Phe Phe Leu Phe Tyr Lys Ala Phe
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Tyr Arg Asn Met Ala Ile Leu Gly Val Glu Gly Phe Ser Ala Leu Pro
545                 550                 555                 560

Gln His Cys Leu Gln Leu Cys Tyr Gly Phe Phe Ala Phe Ala Val Ala
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Ala Asn Leu Val Arg Asp Arg Leu Pro Asp Lys Ile Gly Asn Trp Val
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Pro Leu Pro Met Ala Met Ala Val Pro Phe Leu Val Gly Gly Tyr Phe
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Ala Ile Asp Met Cys Val Gly Ser Leu Ile Val Phe Ala Trp Asn Met
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Arg Asp Arg Val Lys Ala Gly Leu Met Val Pro Ala Val Ala Ser Gly
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Leu Ile Cys Gly Asp Gly Leu Trp Ile Leu Pro Ser Ser Val Leu Ala
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Tyr Ser Ser
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35 40 45

Leu Gly Ser Leu His Tyr His Arg Gln Leu Asn Ile Gly His Glu Pro
50 55 60

Met Leu Lys Asn Gln Asn Pro Asn Asn Ser Ile Phe Gln Asp Phe Leu
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Asn Met Pro Leu Asn Gln Pro Pro Pro Pro Pro Pro Pro Pro Ser Ser
85 90 95

Ser Thr Ile Val Thr Ala Leu Tyr Gly Ser Leu Pro Leu Pro Pro Pro
100 105 110

Ala Thr Val Leu Ser Leu Asn Ser Gly Val Gly Phe Glu Phe Leu Asp
115 120 125

Thr Thr Glu Asn Leu Leu Ala Ser Asn Pro Arg Ser Phe Glu Glu Ser
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Ala Lys Phe Gly Cys Leu Gly Lys Lys Arg Gly Gln Asp Ser Asp Asp
145 150 155 160

Thr Arg Gly Asp Arg Arg Tyr Lys Arg Met Ile Lys Asn Arg Glu Ser
165 170 175

Ala Ala Arg Ser Arg Ala Arg Lys Gln Ala Tyr Thr Asn Glu Leu Glu
180 185 190

Leu Glu Ile Ala His Leu Gln Thr Glu Asn Ala Arg Leu Lys Ile Gln
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<212> PRT
<213> Arabidopsis thaliana

<220>
<223> G270

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            20                  25                  30

Thr Arg Leu Arg Ser Leu Ser Tyr Ser Ser Gln Thr Ser Ile Leu Pro
        35                  40                  45

Asp Ala Gly Asp Asp Phe Ile Val Gly Asp Cys Leu Val Tyr Glu Asp
    50                  55                  60

Gly Val Phe Glu Asp Pro Tyr Leu Asp Lys Glu Val Thr Gln Val Ala
65                  70                  75                  80

Lys Gln Glu Arg Lys Lys Asn Arg Arg Gly Gly Ala Lys Arg Leu Asp
                85                  90                  95

Glu Ser Glu Ile Glu Pro Glu Asn Leu Val Pro Glu Glu Trp Arg Asp
            100                 105                 110

Ile Gln Ala Glu Val Asn Leu Thr Lys Lys Asp Lys Arg Lys Ile Ala
        115                 120                 125

Gln Glu Met Glu Phe Gly Val Arg Val Glu Lys Lys Arg Gln Gly Leu
    130                 135                 140
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Ile Pro Leu Arg Lys Val Asp Leu Asn Asp Phe Leu Thr Tyr Lys Glu
145 150 155 160

Ala Lys Leu Ala Gln Leu Arg Pro Val Ile Leu Asp Lys Pro Gly Asn
165 170 175

Phe Ser Asp Asp Ser Gly Ala Ser Ser Asp Gly Glu Thr Ala Val Ser
180 185 190

Ser Pro Ser Glu Arg Val Ala Pro Lys Asn Pro Arg Trp Ala Val Tyr
195 200 205

Gly Lys Gly Phe Asp His Val Ala Lys Phe Phe Asn Ser Asp Lys Tyr
210 215 220

Asp Pro Ser Asp Lys Lys Ser Asp Gly Pro Arg Lys Leu Leu Ser Lys
225 230 235 240

Glu Glu Lys Phe Met Leu Asn Ser Arg Asn Pro Asp Leu Ala Val Ala
245 250 255

Thr Ser Lys Lys Trp Leu Pro Leu His Thr Leu Ala Ala Cys Gly Glu
260 265 270

Phe Tyr Leu Val Asp Ser Leu Leu Lys His Asn Leu Asp Ile Asn Ala
275 280 285

Thr Asp Val Gly Gly Leu Thr Val Leu His Arg Ala Ile Ile Gly Lys
290 295 300

Lys Gln Ala Ile Thr Asn Tyr Leu Leu Arg Glu Ser Ala Asn Pro Phe
305 310 315 320

Val Leu Asp Asp Glu Gly Ala Thr Leu Met His Tyr Ala Val Gln Thr
325 330 335

Ala Ser Ala Pro Thr Ile Lys Leu Leu Leu Leu Tyr Asn Ala Asp Ile
340 345 350

Asn Ala Gln Asp Arg Asp Gly Trp Thr Pro Leu His Val Ala Val Gln
355 360 365

Ala Arg Arg Ser Asp Ile Val Lys Leu Leu Leu Ile Lys Gly Ala Asp
370 375 380

Ile Glu Val Lys Asn Lys Asp Gly Leu Thr Pro Leu Gly Leu Cys Leu
385 390 395 400

Tyr Leu Gly Arg Glu Ile Arg Thr Tyr Glu Val Met Lys Leu Leu Lys
405 410 415

Glu Phe Pro Leu Ser Arg His Lys Lys Arg Leu Val Thr Thr Asp Glu
420 425 430

Asp Ile Glu
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<212> DNA
<213> Arabidopsis thaliana

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<223> G201

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<212> PRT
<213> Arabidopsis thaliana

<220>
<223> G201

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Gly Gly Gly Gly Trp Arg Asp Ile Pro Gln Lys Ala Gly Leu Lys Arg
35 40 45

Cys Gly Lys Ser Cys Arg Leu Arg Trp Ala Asn Tyr Leu Lys Pro Asp
50 55 60

Ile Lys Arg Gly Glu Phe Ser Tyr Glu Glu Glu Gln Ile Ile Ile Met
65 70 75 80

Leu His Ala Ser Arg Gly Asn Lys Trp Ser Val Ile Ala Arg His Leu
85 90 95

Pro Lys Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr His Leu
100 105 110

Lys Lys Leu Leu Ile Asp Lys Gly Ile Asp Pro Val Thr His Lys Pro
115 120 125

Leu Ala Tyr Asp Ser Asn Pro Asp Glu Gln Ser Gln Ser Gly Ser Ile
130 135 140

Ser Pro Lys Ser Leu Pro Pro Ser Ser Ser Lys Asn Val Pro Glu Ile
145 150 155 160

Thr Ser Ser Asp Glu Thr Pro Lys Tyr Asp Ala Ser Leu Ser Ser Lys
165 170 175

Lys Arg Cys Phe Lys Arg Ser Ser Ser Thr Ser Lys Leu Leu Asn Lys
180 185 190

Val Ala Ala Arg Ala Ser Ser Met Gly Thr Ile Leu Gly Ala Ser Ile
195 200 205

Glu Gly Thr Leu Ile Ser Ser Thr Pro Leu Ser Ser Cys Leu Asn Asp
210 215 220

Asp Phe Ser Glu Thr Ser Gln Phe Gln Met Glu Glu Phe Asp Pro Phe
225 230 235 240

Tyr Gln Ser Ser Glu His Ile Ile Asp His Met Lys Glu Asp Ile Ser
245 250 255

Ile Asn Asn Ser Glu Tyr Asn Phe Ser Gln Phe Leu Glu Gln Phe Ser
260 265 270

Asn Asn Glu Gly Glu Glu Ala Asp Asn Thr Gly Gly Gly Tyr Asn Gln
275 280 285

Asp Leu Leu Met Ser Asp Val Ser Ser Thr Ser Val Asp Glu Asp Glu
290 295 300

Met Met Gln Asn Ile Thr Gly Trp Ser Asn Tyr Leu Leu Asp His Ser
305 310 315 320

Asp Phe Asn Tyr Asp Thr Ser Gln Asp Tyr Asp Asp Lys Asn Phe Ile
325 330 335

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<211> 1651
<212> DNA
<213> Arabidopsis thaliana

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<223> G1417

<400> 59

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20 25 30

Glu Ser Pro Val Glu Arg His His Glu Ser Ser Ile Lys Glu Val Asp
35 40 45

Phe Phe Ala Ala Lys Ser Gln Pro Phe Asp Leu Gly His Val Arg Thr
50 55 60

Thr Thr Ile Val Gly Ser Ser Gly Phe Asn Asp Gly Leu Gly Leu Val
65 70 75 80

Asn Ser Cys His Gly Thr Ser Ser Asn Asp Gly Asp Asp Lys Thr Lys
85 90 95

Thr Gln Ile Ser Arg Leu Lys Leu Glu Leu Glu Arg Leu His Glu Glu
100 105 110

Asn His Lys Leu Lys His Leu Leu Asp Glu Val Ser Glu Ser Tyr Asn
115 120 125

Asp Leu Gln Arg Arg Val Leu Leu Ala Arg Gln Thr Gln Val Glu Gly
130 135 140

Leu His His Lys Gln His Glu Asp Val Pro Gln Ala Gly Ser Ser Gln
145 150 155 160

Ala Leu Glu Asn Arg Arg Pro Lys Asp Met Asn His Glu Thr Pro Ala
165 170 175

Thr Thr Leu Lys Arg Arg Ser Pro Asp Asp Val Asp Gly Arg Asp Met
180 185 190

His Arg Gly Ser Pro Lys Thr Pro Arg Ile Asp Gln Asn Lys Ser Thr
195 200 205

Asn His Glu Glu Gln Gln Asn Pro His Asp Gln Leu Pro Tyr Arg Lys
210 215 220

Ala Arg Val Ser Val Arg Ala Arg Ser Asp Ala Thr Thr Val Asn Asp
225 230 235 240

Gly Cys Gln Trp Arg Lys Tyr Gly Gln Lys Met Ala Lys Gly Asn Pro
245 250 255

Cys Pro Arg Ala Tyr Tyr Arg Cys Thr Met Ala Val Gly Cys Pro Val
260 265 270

Arg Lys Gln Val Gln Arg Cys Ala Glu Asp Thr Thr Ile Leu Thr Thr
275 280 285

Thr Tyr Glu Gly Asn His Asn His Pro Leu Pro Pro Ser Ala Thr Ala
290 295 300

Met Ala Ala Thr Thr Ser Ala Ala Ala Ala Met Leu Leu Ser Gly Ser
305 310 315 320

Ser Ser Ser Asn Leu His Gln Thr Leu Ser Ser Pro Ser Ala Thr Ser
325 330 335

Ser Ser Ser Phe Tyr His Asn Phe Pro Tyr Thr Ser Thr Ile Ala Thr
340 345 350

Leu Ser Ala Ser Ala Pro Phe Pro Thr Ile Thr Leu Asp Leu Thr Asn
355 360 365

Pro Pro Arg Pro Leu Gln Pro Pro Pro Gln Phe Leu Ser Gln Tyr Gly
370 375 380

Pro Ala Ala Phe Leu Pro Asn Ala Asn Gln Ile Arg Ser Met Asn Asn
385 390 395 400

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Asn Asn Gln Gln Leu Leu Ile Pro Asn Leu Phe Gly Pro Gln Ala Pro
                405                 410                 415

Pro Arg Glu Met Val Asp Ser Val Arg Ala Ala Ile Ala Met Asp Pro
            420                 425                 430

Asn Phe Thr Ala Ala Leu Ala Ala Ala Ile Ser Asn Ile Ile Gly Gly
        435                 440                 445

Gly Asn Asn Asp Asn Asn Asn Asn Thr Asp Ile Asn Asp Asn Lys Val
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Asp Ala Lys Ser Gly Gly Ser Ser Asn Gly Asp Ser Pro Gln Leu Pro
465                 470                 475                 480

Gln Ser Cys Thr Thr Phe Ser Thr Asn
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<212> DNA
<213> Arabidopsis thaliana

<220>
<223> G233

<400> 61

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<213> Arabidopsis thaliana

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20 25 30

Gly His Ser Asn Trp Arg Ala Leu Pro Lys Gln Ala Gly Leu Leu Arg
35 40 45

Cys Gly Lys Ser Cys Arg Leu Arg Trp Met Asn Tyr Leu Lys Pro Asp
50 55 60

Ile Lys Arg Gly Asn Phe Thr Lys Glu Glu Glu Asp Ala Ile Ile Ser
65 70 75 80

Leu His Gln Ile Leu Gly Asn Arg Trp Ser Ala Ile Ala Ala Lys Leu
85 90 95

Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Val Trp His Thr His Leu
100 105 110

Lys Lys Arg Leu Glu Asp Tyr Gln Pro Ala Lys Pro Lys Thr Ser Asn
115 120 125

Lys Lys Lys Gly Thr Lys Pro Lys Ser Glu Ser Val Ile Thr Ser Ser
130 135 140

Asn Ser Thr Arg Ser Glu Ser Glu Leu Ala Asp Ser Ser Asn Pro Ser
145 150 155 160

Gly Glu Ser Leu Phe Ser Thr Ser Pro Ser Thr Ser Glu Val Ser Ser
165 170 175

Met Thr Leu Ile Ser His Asp Gly Tyr Ser Asn Glu Ile Asn Met Asp
180 185 190

Asn Lys Pro Gly Asp Ile Ser Thr Ile Asp Gln Glu Cys Val Ser Phe
195 200 205

Glu Thr Phe Gly Ala Asp Ile Asp Glu Ser Phe Trp Lys Glu Thr Leu
210 215 220

Tyr Ser Gln Asp Glu His Asn Tyr Val Ser Asn Asp Leu Glu Val Ala
225 230 235 240

Gly Leu Val Glu Ile Gln Gln Glu Phe Gln Asn Leu Gly Ser Ala Asn
245 250 255

Asn Glu Met Ile Phe Asp Ser Glu Met Glu Leu Leu Val Arg Cys Ile
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<212> DNA
<213> Arabidopsis thaliana

<220>
<223> G920

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<212> PRT
<213> Arabidopsis thaliana

<220>
<223> G920

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            20   25   30

Leu Ser His Gln His Ser Asn Gln Tyr His Ile Asp Glu Thr Arg Leu
        35   40   45

Val Ser Gly Ser Gly Ser Val Ser Gly Gly Pro Asp Pro Val Asp Glu
    50   55   60

Leu Met Ser Lys Ile Leu Gly Ser Phe His Lys Thr Ile Ser Val Leu
65   70   75   80

Asp Ser Phe Asp Pro Val Ala Val Ser Val Pro Ile Ala Val Glu Gly
                85   90   95

Ser Trp Asn Ala Ser Cys Gly Asp Asp Ser Ala Thr Pro Val Ser Cys
            100   105   110

Asn Gly Gly Asp Ser Gly Glu Ser Lys Lys Lys Arg Leu Gly Val Gly
        115   120   125

Lys Gly Lys Arg Gly Cys Tyr Thr Arg Lys Thr Arg Ser His Thr Arg
    130   135   140

Ile Val Glu Ala Lys Ser Ser Glu Asp Arg Tyr Ala Trp Arg Lys Tyr
145   150   155   160

Gly Gln Lys Glu Ile Leu Asn Thr Thr Phe Pro Arg Ser Tyr Phe Arg
                165   170   175

Cys Thr His Lys Pro Thr Gln Gly Cys Lys Ala Thr Lys Gln Val Gln
            180   185   190

Lys Gln Asp Gln Asp Ser Glu Met Phe Gln Ile Thr Tyr Ile Gly Tyr
        195   200   205

His Thr Cys Thr Ala Asn Asp Gln Thr His Ala Lys Thr Glu Pro Phe
    210   215   220

Asp Gln Glu Ile Ile Met Asp Ser Glu Lys Thr Leu Ala Ala Ser Thr
225   230   235   240

Ala Gln Asn His Val Asn Ala Met Val Gln Glu Gln Glu Asn Asn Thr
                245   250   255

Ser Ser Val Thr Ala Ile Asp Ala Gly Met Val Lys Glu Glu Gln Asn
            260   265   270

Asn Asn Gly Asp Gln Ser Lys Asp Tyr Tyr Glu Gly Ser Ser Thr Gly
        275   280   285

Glu Asp Leu Ser Leu Val Trp Gln Glu Thr Met Met Phe Asp Asp His
    290   295   300

Gln Asn His Tyr Tyr Cys Gly Glu Thr Ser Thr Thr Ser His Gln Phe
305   310   315   320

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Cys Ala Asp Tyr Glu Arg Thr Ser Ala Met
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<212> DNA
<213> Arabidopsis thaliana

<220>
<223> G867

<400> 65

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caggatcaac agttgtacat tgggtggaag tcgagatccg ggtcagattt agatgcgggt 960
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<211> 344
<212> PRT
<213> Arabidopsis thaliana

<220>
<223> G867

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Cys Glu Thr Pro Ala Ile Thr Pro Ala Lys Lys Ser Ser Val Gly Asn
20 25 30

Leu Tyr Arg Met Gly Ser Gly Ser Ser Val Val Leu Asp Ser Glu Asn
35 40 45

Gly Val Glu Ala Glu Ser Arg Lys Leu Pro Ser Ser Lys Tyr Lys Gly
50 55 60

Val Val Pro Gln Pro Asn Gly Arg Trp Gly Ala Gln Ile Tyr Glu Lys
65 70 75 80

His Gln Arg Val Trp Leu Gly Thr Phe Asn Glu Glu Asp Glu Ala Ala
85 90 95

Arg Ala Tyr Asp Val Ala Val His Arg Phe Arg Arg Arg Asp Ala Val
100 105 110

Thr Asn Phe Lys Asp Val Lys Met Asp Glu Asp Glu Val Asp Phe Leu
115 120 125

Asn Ser His Ser Lys Ser Glu Ile Val Asp Met Leu Arg Lys His Thr
130 135 140

Tyr Asn Glu Glu Leu Glu Gln Ser Lys Arg Arg Arg Asn Gly Asn Gly
145 150 155 160

Asn Met Thr Arg Thr Leu Leu Thr Ser Gly Leu Ser Asn Asp Gly Val
165 170 175

Ser Thr Thr Gly Phe Arg Ser Ala Glu Ala Leu Phe Glu Lys Ala Val
180 185 190

Thr Pro Ser Asp Val Gly Lys Leu Asn Arg Leu Val Ile Pro Lys His
195 200 205

His Ala Glu Lys His Phe Pro Leu Pro Ser Ser Asn Val Ser Val Lys
210 215 220

Gly Val Leu Leu Asn Phe Glu Asp Val Asn Gly Lys Val Trp Arg Phe
225 230 235 240

Arg Tyr Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Leu Thr Lys Gly
245 250 255

Trp Ser Arg Phe Val Lys Glu Lys Asn Leu Arg Ala Gly Asp Val Val
260 265 270

Ser Phe Ser Arg Ser Asn Gly Gln Asp Gln Gln Leu Tyr Ile Gly Trp
275 280 285

Lys Ser Arg Ser Gly Ser Asp Leu Asp Ala Gly Arg Val Leu Arg Leu
290 295 300

Phe Gly Val Asn Ile Ser Pro Glu Ser Ser Arg Asn Asp Val Val Gly
305 310 315 320

Asn Lys Arg Val Asn Asp Thr Glu Met Leu Ser Leu Val Cys Ser Lys
325 330 335

Lys Gln Arg Ile Phe His Ala Ser
340

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<211> 984
<212> DNA
<213> Arabidopsis thaliana

<220>
<223> G659

<400> 67
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tctctcccca aacaatctgg tatgtcattg cttttgtcat cacaatcaaa gcaaaagcct 180
cttcaattgt tttttctttt ctttatgatt ctgaatgtat atatatgcaa aaatgaaggg 240
ctattgaggt gtgggaagag ttgtcgtcta aggtggatta actatcttag gccagatctg 300
aagcgtggca acttcacttc agaggaggaa gaaacaatca ttaagcttca ccacaactat 360

gggaacaagt ggtcgaaaat cgcttctcaa cttccaggta gaacagataa cgagatcaag 420
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ccggcctcgc cttgttcgag tgattctgtt tctcgtggga aagatgataa gtcatctcac 540
gtagaagatt ctttgaacag agagactaat cataggaatg agttgtctac atctatgtct 600
tctggggggtt ccaaccaaca agatgatcca aagatagacg aactcaggtt tgagtatata 660
gaagaagctt atagcgagtt taacgacatt attattcaag aggtagacaa acccgatctg 720
ctggagatac catttgattc agatcctgac atttggagtt tcttagatac ttcaaactca 780
tttcaacaat ccactgcaaa tgagaacagc tcaggctcaa gagcaacaac agaagaagag 840
tctgatgagg atgaggttaa gaaatggttc aagcacctag aaagcgaact cgggttagaa 900
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aactacgagc tcatgataca ttga 984

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<211> 327
<212> PRT
<213> Arabidopsis thaliana

<220>
<223> G659

<400> 68
Met Gly Lys Gly Arg Ala Pro Cys Cys Asp Lys Thr Lys Val Lys Arg
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Gly Pro Trp Ser Pro Glu Glu Asp Ile Lys Leu Ile Ser Phe Ile Gln
20 25 30

Lys Phe Gly His Glu Asn Trp Arg Ser Leu Pro Lys Gln Ser Gly Met
35 40 45

Ser Leu Leu Leu Ser Ser Gln Ser Lys Gln Lys Pro Leu Gln Leu Phe
50 55 60

Phe Leu Phe Phe Met Ile Leu Asn Val Tyr Ile Cys Lys Asn Glu Gly
65 70 75 80

Leu Leu Arg Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu
85 90 95

Arg Pro Asp Leu Lys Arg Gly Asn Phe Thr Ser Glu Glu Glu Glu Thr
100 105 110

Ile Ile Lys Leu His His Asn Tyr Gly Asn Lys Trp Ser Lys Ile Ala
115 120 125

Ser Gln Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Val Trp His
130 135 140

Thr His Leu Lys Lys Arg Leu Ala Gln Ser Ser Gly Thr Ala Asp Glu
145 150 155 160

Pro Ala Ser Pro Cys Ser Ser Asp Ser Val Ser Arg Gly Lys Asp Asp
165 170 175

Lys Ser Ser His Val Glu Asp Ser Leu Asn Arg Glu Thr Asn His Arg
180 185 190

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Asn Glu Leu Ser Thr Ser Met Ser Ser Gly Gly Ser Asn Gln Gln Asp
        195                 200                 205

Asp Pro Lys Ile Asp Glu Leu Arg Phe Glu Tyr Ile Glu Glu Ala Tyr
    210                 215                 220

Ser Glu Phe Asn Asp Ile Ile Ile Gln Glu Val Asp Lys Pro Asp Leu
225                 230                 235                 240

Leu Glu Ile Pro Phe Asp Ser Asp Pro Asp Ile Trp Ser Phe Leu Asp
                245                 250                 255

Thr Ser Asn Ser Phe Gln Gln Ser Thr Ala Asn Glu Asn Ser Ser Gly
            260                 265                 270

Ser Arg Ala Thr Thr Glu Glu Glu Ser Asp Glu Asp Glu Val Lys Lys
        275                 280                 285

Trp Phe Lys His Leu Glu Ser Glu Leu Gly Leu Glu Glu Asp Asp Asn
    290                 295                 300

Gln Gln Gln Tyr Lys Glu Glu Glu Ser Ser Ser Ser Ser Leu Leu Lys
305                 310                 315                 320

Asn Tyr Glu Leu Met Ile His
                325


<210> 69
<211> 826
<212> DNA
<213> Arabidopsis thaliana

<220>
<223> G620

<400> 69
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cgtgagcaag accaatacat gccaatcgca aacgtcataa gaatcatgcg taaaacctta 180
ccgtctcacg ccaaaatctc tgacgacgcc aaagaaacga ttcaagaatg tgtctccgag 240
tacatcagct tcgtgaccgg tgaagccaac gagcgttgcc aacgtgagca acgtaagacc 300
ataactgctg aagatatcct ttgggctatg agcaagcttg ggttcgataa ctacgtggac 360
cccctcaccg tgttcattaa ccggtaccgt gagatagaga ccgatcgtgg ttctgcactt 420
agaggtgagc caccgtcgtt gagacaaacc tatggaggaa atggtattgg gtttcacggc 480
ccatctcatg gcctacctcc tccgggtcct tatggttatg gtatgttgga ccaatccatg 540
gttatgggag gtggtcggta ctaccaaaac gggtcgtcgg gtcaagatga atccagtgtt 600
ggtggtggct cttcgtcttc cattaacgga atgccggctt ttgaccatta tggtcagtat 660
aagtgaagaa ggagttattc ttcattttta tatctattca aaacatgtgt ttcgatagat 720
attttatttt tatgtcttat caataacatt tctatataat gttgcttctt taaggaaaag 780
tgttgtatgt caatacttta tgagaaactg atttatatat gcaaat                826


<210> 70
<211> 208
<212> PRT
<213> Arabidopsis thaliana
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<220>
<223> G620

<400> 70
Met Thr Ser Ser Val Ile Val Ala Gly Ala Gly Asp Lys Asn Asn Gly
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Ile Val Val Gln Gln Gln Pro Pro Cys Val Ala Arg Glu Gln Asp Gln
20 25 30

Tyr Met Pro Ile Ala Asn Val Ile Arg Ile Met Arg Lys Thr Leu Pro
35 40 45

Ser His Ala Lys Ile Ser Asp Asp Ala Lys Glu Thr Ile Gln Glu Cys
50 55 60

Val Ser Glu Tyr Ile Ser Phe Val Thr Gly Glu Ala Asn Glu Arg Cys
65 70 75 80

Gln Arg Glu Gln Arg Lys Thr Ile Thr Ala Glu Asp Ile Leu Trp Ala
85 90 95

Met Ser Lys Leu Gly Phe Asp Asn Tyr Val Asp Pro Leu Thr Val Phe
100 105 110

Ile Asn Arg Tyr Arg Glu Ile Glu Thr Asp Arg Gly Ser Ala Leu Arg
115 120 125

Gly Glu Pro Pro Ser Leu Arg Gln Thr Tyr Gly Gly Asn Gly Ile Gly
130 135 140

Phe His Gly Pro Ser His Gly Leu Pro Pro Pro Gly Pro Tyr Gly Tyr
145 150 155 160

Gly Met Leu Asp Gln Ser Met Val Met Gly Gly Gly Arg Tyr Tyr Gln
165 170 175

Asn Gly Ser Ser Gly Gln Asp Glu Ser Ser Val Gly Gly Gly Ser Ser
180 185 190

Ser Ser Ile Asn Gly Met Pro Ala Phe Asp His Tyr Gly Gln Tyr Lys
195 200 205

<210> 71
<211> 1394
<212> DNA
<213> Arabidopsis thaliana

<220>
<223> G596

<400> 71
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attagggttt caattgttta ctttttgttt gctttttata tcaagtaatg gatcaggtct 180
ctcgctctct tcctccacct tttctctcaa gagatctcca tcttcaccca caccatcaat 240
tccagcatca gcagcagcag cagcaacaga atcacggcca cgatatagac cagcaccgaa 300

tcggtgggct aaaacgtgac cgagatgctg atatcgatcc caacgagcac tcttcagccg 360
gaaaagatca aagtactcct ggctccggtg gagaaagcgg cggcggagga ggaggagata 420
atcacatcac gagaaggcca cgtggcagac cagcgggatc taagaacaaa ccaaaaccgc 480
caatcatcat cactcgagac agcgcaaacg ctctcaaatc tcatgtcatg gaagtagcaa 540
acggatgtga cgtcatggaa agtgtcaccg tcttcgctcg ccgtcgccaa cgtggcatct 600
gcgttttgag cggaaacggc gccgttacca acgttaccat aagacaacca gcttcagtac 660
ctggtggtgg ctcatctgtc gttaacttac acggacgttt cgagattctt tctctctcgg 720
gatcattcct tcctcctccg gctccaccag ctgcgtcagg tctaacgatt tacttagccg 780
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cagctgaagc ttattgggga actccgagac catctttcta aatcgcgaag aaaaaacaag 1140
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gaatcgaaga gaatcgtttt ggtcatggga ttgctcgatc tattaggttt gagagggggt 1320
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<210> 72
<211> 317
<212> PRT
<213> Arabidopsis thaliana

<220>
<223> G596

<400> 72
Met Asp Gln Val Ser Arg Ser Leu Pro Pro Pro Phe Leu Ser Arg Asp
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Leu His Leu His Pro His His Gln Phe Gln His Gln Gln Gln Gln Gln
20 25 30

Gln Gln Asn His Gly His Asp Ile Asp Gln His Arg Ile Gly Gly Leu
35 40 45

Lys Arg Asp Arg Asp Ala Asp Ile Asp Pro Asn Glu His Ser Ser Ala
50 55 60

Gly Lys Asp Gln Ser Thr Pro Gly Ser Gly Gly Glu Ser Gly Gly Gly
65 70 75 80

Gly Gly Gly Asp Asn His Ile Thr Arg Arg Pro Arg Gly Arg Pro Ala
85 90 95

Gly Ser Lys Asn Lys Pro Lys Pro Pro Ile Ile Ile Thr Arg Asp Ser
100 105 110

Ala Asn Ala Leu Lys Ser His Val Met Glu Val Ala Asn Gly Cys Asp
115 120 125

Val Met Glu Ser Val Thr Val Phe Ala Arg Arg Arg Gln Arg Gly Ile
130 135 140

Cys Val Leu Ser Gly Asn Gly Ala Val Thr Asn Val Thr Ile Arg Gln
145 150 155 160

Pro Ala Ser Val Pro Gly Gly Gly Ser Ser Val Val Asn Leu His Gly
165 170 175

Arg Phe Glu Ile Leu Ser Leu Ser Gly Ser Phe Leu Pro Pro Pro Ala
180 185 190

Pro Pro Ala Ala Ser Gly Leu Thr Ile Tyr Leu Ala Gly Gly Gln Gly
195 200 205

Gln Val Val Gly Gly Ser Val Val Gly Pro Leu Met Ala Ser Gly Pro
210 215 220

Val Val Ile Met Ala Ala Ser Phe Gly Asn Ala Ala Tyr Glu Arg Leu
225 230 235 240

Pro Leu Glu Glu Asp Asp Gln Glu Glu Gln Thr Ala Gly Ala Val Ala
245 250 255

Asn Asn Ile Asp Gly Asn Ala Thr Met Gly Gly Gly Thr Gln Thr Gln
260 265 270

Thr Gln Thr Gln Gln Gln Gln Gln Gln Gln Leu Met Gln Asp Pro Thr
275 280 285

Ser Phe Ile Gln Gly Leu Pro Pro Asn Leu Met Asn Ser Val Gln Leu
290 295 300

Pro Ala Glu Ala Tyr Trp Gly Thr Pro Arg Pro Ser Phe
305 310 315

<210> 73
<211> 913
<212> DNA
<213> Arabidopsis thaliana

<220>
<223> G511

<400> 73
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agtgatgact caatgcatcg tgtcattccc gtacttgacg tctttgaggt cgagcctagt 180
catcttccaa atgttgctgg agtgagatgt cgaggagacg ctgagcaatg gttcttcttc 240
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tactggaaag caactggatc acctggtcca gtcttttcca aagacaacaa aatgattgga 360
gcaaagaaaa ctatggtttt ctacactgga aaagcaccca caggaagaaa aactaaatgg 420
aaaatgaatg agtaccacgc cgttgacgaa acagtcaacg cttccacaat ccctaagctg 480
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gagacatcgt tccgtgtgga aagctcactg gaaacttcga tttcaggagg agaacatatt 660
gatgtctcta tgaacacaga gtttgttgat ggactatcag aaccgatgtg ggactgggaa 720
cagctgactt ggccttgaag ctatatagat tttataatca agcaaattta aacttgtttc 780
aattgcttat tgttagtttg aattttatga cccgaaagat tctttttctt tctttacctt 840
gtaacgtgag aatttgagaa ataataaatg acctagacag tgacatttga aaaaaaaaaa 900

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<210> 74
<211> 235
<212> PRT
<213> Arabidopsis thaliana

<220>
<223> G511

<400> 74
Met Ala Asp Glu Val Thr Ile Gly Phe Arg Phe Tyr Pro Thr Glu Glu
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Glu Leu Val Ser Phe Tyr Leu Arg Asn Gln Leu Glu Gly Arg Ser Asp
20 25 30

Asp Ser Met His Arg Val Ile Pro Val Leu Asp Val Phe Glu Val Glu
35 40 45

Pro Ser His Leu Pro Asn Val Ala Gly Val Arg Cys Arg Gly Asp Ala
50 55 60

Glu Gln Trp Phe Phe Phe Val Pro Arg Gln Glu Arg Glu Ala Arg Gly
65 70 75 80

Gly Arg Pro Ser Arg Thr Thr Gly Ser Gly Tyr Trp Lys Ala Thr Gly
85 90 95

Ser Pro Gly Pro Val Phe Ser Lys Asp Asn Lys Met Ile Gly Ala Lys
100 105 110

Lys Thr Met Val Phe Tyr Thr Gly Lys Ala Pro Thr Gly Arg Lys Thr
115 120 125

Lys Trp Lys Met Asn Glu Tyr His Ala Val Asp Glu Thr Val Asn Ala
130 135 140

Ser Thr Ile Pro Lys Leu Arg Arg Glu Phe Ser Leu Cys Arg Val Tyr
145 150 155 160

Ile Thr Thr Gly Ser Ser Arg Ala Phe Asp Arg Arg Pro Glu Gly Val
165 170 175

Leu Gln Thr Glu Arg Met Leu Thr Ser Asp Val Ala Val Ala Glu Thr
180 185 190

Ser Phe Arg Val Glu Ser Ser Leu Glu Thr Ser Ile Ser Gly Gly Glu
195 200 205

His Ile Asp Val Ser Met Asn Thr Glu Phe Val Asp Gly Leu Ser Glu
210 215 220

Pro Met Trp Asp Trp Glu Gln Leu Thr Trp Pro
225 230 235

<210> 75
<211> 2332
<212> DNA
<213> Arabidopsis thaliana

<220>
<223> G471

<400> 75
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caaagcgaac ccactagccc agatgcccct gttcaagaac ctgaaaagtg caccgtacat 480
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<210> 76
<211> 665
<212> PRT
<213> Arabidopsis thaliana

<220>
<223> G471

<400> 76

Met Ala Ala Ser Asn His Ser Ser Gly Lys Pro Gly Gly Val Leu Ser
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Asp Ala Leu Cys Arg Glu Leu Trp His Ala Cys Ala Gly Pro Leu Val
            20   25   30

Thr Leu Pro Arg Glu Gly Glu Arg Val Tyr Tyr Phe Pro Glu Gly His
        35   40   45

Met Glu Gln Leu Glu Ala Ser Met His Gln Gly Leu Glu Gln Gln Met
    50   55   60

Pro Ser Phe Asn Leu Pro Ser Lys Ile Leu Cys Lys Val Ile Asn Ile
65   70   75   80

Gln Arg Arg Ala Glu Pro Glu Thr Asp Glu Val Tyr Ala Gln Ile Thr
                85   90   95

Leu Leu Pro Glu Leu Asp Gln Ser Glu Pro Thr Ser Pro Asp Ala Pro
            100   105   110

Val Gln Glu Pro Glu Lys Cys Thr Val His Ser Phe Cys Lys Thr Leu
        115   120   125

Thr Ala Ser Asp Thr Ser Thr His Gly Gly Phe Ser Val Leu Arg Arg
    130   135   140

His Ala Asp Asp Cys Leu Pro Pro Leu Asp Met Ser Gln Gln Pro Pro
145   150   155   160

Trp Gln Glu Leu Val Ala Thr Asp Leu His Asn Ser Glu Trp His Phe
                165   170   175

Arg His Ile Phe Arg Gly Gln Pro Arg Arg His Leu Leu Thr Thr Gly
            180   185   190

Trp Ser Val Phe Val Ser Ser Lys Lys Leu Val Ala Gly Asp Ala Phe
        195   200   205

Ile Phe Leu Arg Gly Glu Asn Glu Glu Leu Arg Val Gly Val Arg Arg
    210   215   220

His Met Arg Gln Gln Thr Asn Ile Pro Ser Ser Val Ile Ser Ser His
225   230   235   240

Ser Met His Ile Gly Val Leu Ala Thr Ala Ala His Ala Ile Thr Thr
                245   250   255

Gly Thr Ile Phe Ser Val Phe Tyr Lys Pro Arg Thr Ser Arg Ser Glu
            260   265   270

Phe Ile Val Ser Val Asn Arg Tyr Leu Glu Ala Lys Thr Gln Lys Leu
        275   280   285

Ser Val Gly Met Arg Phe Lys Met Arg Phe Glu Gly Glu Glu Ala Pro
    290   295   300

Glu Lys Arg Phe Ser Gly Thr Ile Val Gly Val Gln Glu Asn Lys Ser
305 310 315 320

Ser Val Trp His Asp Ser Glu Trp Arg Ser Leu Lys Val Gln Trp Asp
325 330 335

Glu Pro Ser Ser Val Phe Arg Pro Glu Arg Val Ser Pro Trp Glu Leu
340 345 350

Glu Pro Leu Val Ala Asn Ser Thr Pro Ser Ser Gln Pro Gln Pro Pro
355 360 365

Gln Arg Asn Lys Arg Pro Arg Pro Pro Gly Leu Pro Ser Pro Ala Thr
370 375 380

Gly Pro Ser Gly Pro Val Thr Pro Asp Gly Val Trp Lys Ser Pro Ala
385 390 395 400

Asp Thr Pro Ser Ser Val Pro Leu Phe Ser Pro Pro Ala Lys Ala Ala
405 410 415

Thr Phe Gly His Gly Gly Asn Lys Ser Phe Gly Val Ser Ile Gly Ser
420 425 430

Ala Phe Trp Pro Thr Asn Ala Asp Ser Ala Ala Glu Ser Phe Ala Ser
435 440 445

Ala Phe Asn Asn Glu Ser Thr Glu Lys Lys Gln Thr Asn Gly Asn Val
450 455 460

Cys Arg Leu Phe Gly Phe Glu Leu Val Glu Asn Val Asn Val Asp Glu
465 470 475 480

Cys Phe Ser Ala Ala Ser Val Ser Gly Ala Val Ala Val Asp Gln Pro
485 490 495

Val Pro Ser Asn Glu Phe Asp Ser Gly Gln Gln Ser Glu Pro Leu Asn
500 505 510

Ile Asn Gln Ser Asp Ile Pro Ser Gly Ser Gly Asp Pro Glu Lys Ser
515 520 525

Ser Leu Arg Ser Pro Gln Glu Ser Gln Ser Arg Gln Ile Arg Ser Cys
530 535 540

Thr Lys Val His Met Gln Gly Ser Ala Val Gly Arg Ala Ile Asp Leu
545 550 555 560

Thr Arg Ser Glu Cys Tyr Glu Asp Leu Phe Lys Lys Leu Glu Glu Met
565 570 575

Phe Asp Ile Lys Gly Glu Leu Leu Glu Ser Thr Lys Lys Trp Gln Val
580 585 590

Val Tyr Thr Asp Asp Glu Asp Asp Met Met Met Val Gly Asp Asp Pro
595 600 605

Trp Asn Glu Phe Cys Gly Met Val Arg Lys Ile Phe Ile Tyr Thr Pro
    610   615   620

Glu Glu Val Lys Lys Leu Ser Pro Lys Asn Lys Leu Ala Val Asn Ala
625   630   635   640

Arg Met Gln Leu Lys Ala Asp Ala Glu Glu Asn Gly Asn Thr Glu Gly
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Arg Ser Ser Ser Met Ala Gly Ser Arg
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<212> DNA
<213> Arabidopsis thaliana

<220>
<223> G385

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cctacggcta agctgtctct tggctctgtt gcaactgtca ataatctaat agcttgcact 2160

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<211> 721
<212> PRT
<213> Arabidopsis thaliana

<220>
<223> G385

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Arg Asp Asp Glu Phe Asp Ser Pro Asn Thr Lys Ser Gly Ser Glu Asn
35 40 45

Gln Glu Gly Gly Ser Gly Asn Asp Gln Asp Pro Leu His Pro Asn Lys
50 55 60

Lys Lys Arg Tyr His Arg His Thr Gln Leu Gln Ile Gln Glu Met Glu
65 70 75 80

Ala Phe Phe Lys Glu Cys Pro His Pro Asp Asp Lys Gln Arg Lys Gln
85 90 95

Leu Ser Arg Glu Leu Asn Leu Glu Pro Leu Gln Val Lys Phe Trp Phe
100 105 110

Gln Asn Lys Arg Thr Gln Met Lys Asn His His Glu Arg His Glu Asn
115 120 125

Ser His Leu Arg Ala Glu Asn Glu Lys Leu Arg Asn Asp Asn Leu Arg
130 135 140

Tyr Arg Glu Ala Leu Ala Asn Ala Ser Cys Pro Asn Cys Gly Gly Pro
145 150 155 160

Thr Ala Ile Gly Glu Met Ser Phe Asp Glu His Gln Leu Arg Leu Glu
165 170 175

Asn Ala Arg Leu Arg Glu Glu Ile Asp Arg Ile Ser Ala Ile Ala Ala
180 185 190

Lys Tyr Val Gly Lys Pro Val Ser Asn Tyr Pro Leu Met Ser Pro Pro
195 200 205

Pro Leu Pro Pro Arg Pro Leu Glu Leu Ala Met Gly Asn Ile Gly Gly
210 215 220

Glu Ala Tyr Gly Asn Asn Pro Asn Asp Leu Leu Lys Ser Ile Thr Ala
225 230 235 240

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Pro Thr Glu Ser Asp Lys Pro Val Ile Ile Asp Leu Ser Val Ala Ala
                245                 250                 255

Met Glu Glu Leu Met Arg Met Val Gln Val Asp Glu Pro Leu Trp Lys
            260                 265                 270

Ser Leu Ala Leu Asp Glu Glu Glu Tyr Ala Arg Thr Phe Pro Arg Gly
        275                 280                 285

Ile Gly Pro Arg Pro Ala Gly Tyr Arg Ser Glu Ala Ser Arg Glu Ser
    290                 295                 300

Ala Val Val Ile Met Asn His Val Asn Ile Val Glu Ile Leu Met Asp
305                 310                 315                 320

Val Asn Gln Trp Ser Thr Ile Phe Ala Gly Met Val Ser Arg Ala Met
                325                 330                 335

Thr Leu Ala Val Leu Ser Thr Gly Val Ala Gly Asn Tyr Asn Gly Ala
            340                 345                 350

Leu Gln Val Met Ser Ala Glu Phe Gln Val Pro Ser Pro Leu Val Pro
        355                 360                 365

Thr Arg Glu Thr Tyr Phe Ala Arg Tyr Cys Lys Gln Gln Gly Asp Gly
    370                 375                 380

Ser Trp Ala Val Val Asp Ile Ser Leu Asp Ser Leu Gln Pro Asn Pro
385                 390                 395                 400

Pro Ala Arg Cys Arg Arg Arg Ala Ser Gly Cys Leu Ile Gln Glu Leu
                405                 410                 415

Pro Asn Gly Tyr Ser Lys Val Thr Trp Val Glu His Val Glu Val Asp
            420                 425                 430

Asp Arg Gly Val His Asn Leu Tyr Lys His Met Val Ser Thr Gly His
        435                 440                 445

Ala Phe Gly Ala Lys Arg Trp Val Ala Ile Leu Asp Arg Gln Cys Glu
    450                 455                 460

Arg Leu Ala Ser Val Met Ala Thr Asn Ile Ser Ser Gly Glu Val Gly
465                 470                 475                 480

Val Ile Thr Asn Gln Glu Gly Arg Arg Ser Met Leu Lys Leu Ala Glu
                485                 490                 495

Arg Met Val Ile Ser Phe Cys Ala Gly Val Ser Ala Ser Thr Ala His
            500                 505                 510

Thr Trp Thr Thr Leu Ser Gly Thr Gly Ala Glu Asp Val Arg Val Met
        515                 520                 525

Thr Arg Lys Ser Val Asp Asp Pro Gly Arg Ser Pro Gly Ile Val Leu
    530                 535                 540
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Ser Ala Ala Thr Ser Phe Trp Ile Pro Val Pro Pro Lys Arg Val Phe
545 550 555 560

Asp Phe Leu Arg Asp Glu Asn Ser Arg Asn Glu Trp Asp Ile Leu Ser
565 570 575

Asn Gly Gly Val Val Gln Glu Met Ala His Ile Ala Asn Gly Arg Asp
580 585 590

Thr Gly Asn Cys Val Ser Leu Leu Arg Val Asn Ser Ala Asn Ser Ser
595 600 605

Gln Ser Asn Met Leu Ile Leu Gln Glu Ser Cys Ile Asp Pro Thr Ala
610 615 620

Ser Phe Val Ile Tyr Ala Pro Val Asp Ile Val Ala Met Asn Ile Val
625 630 635 640

Leu Asn Gly Gly Asp Pro Asp Tyr Val Ala Leu Leu Pro Ser Gly Phe
645 650 655

Ala Ile Leu Pro Asp Gly Asn Ala Asn Ser Gly Ala Pro Gly Gly Asp
660 665 670

Gly Gly Ser Leu Leu Thr Val Ala Phe Gln Ile Leu Val Asp Ser Val
675 680 685

Pro Thr Ala Lys Leu Ser Leu Gly Ser Val Ala Thr Val Asn Asn Leu
690 695 700

Ile Ala Cys Thr Val Glu Arg Ile Lys Ala Ser Met Ser Cys Glu Thr
705 710 715 720

Ala

<210> 79
<211> 1857
<212> DNA
<213> Arabidopsis thaliana

<220>
<223> G261

<400> 79
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gcttttgctt gattgtcttt tatttagaaa cagtggtgag tttttagtct ttcactttgt 180
tcaagttcga agcttttttt ggagggaatt ttgggcttct gattttgatc gaaacttact 240
gatagtaagt tctttgagtc ctccttaact gtagtttctg tgtactgaag ttattgaatt 300
gaaagttttt atcttttttg gttattgaaa ctttcatagt ttgatcaaaa gagtctcttg 360
ctctgttttt ggctctgttt ttgtgagtgt gattgtaagc tttgttgtga gtagattgaa 420
tcaaggagtg tgagagttgt taaaagtgtt ttcagagatg gatgagaata atcatggagt 480
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ggagttttct agagatcttc ttccgagatt cttcaagcac aataacttct ctagctttat 660
ccgccagctt aacacatatg gttttagaaa agctgatcct gagcaatggg aatttgcgaa 720

tgatgatttt gtgagaggtc aacctcatct tatgaagaac attcatagac gcaaaccagt 780
tcatagccac tctttaccga atcttcaagc tcagttaaac ccgttgacgg attcagaacg 840
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gttacataaa caagacgagg aacgagaagt gtttgagatg caagtgaaag aacttaaaga 960
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<211> 401
<212> PRT
<213> Arabidopsis thaliana

<220>
<223> G261

<400> 80
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Leu Thr Lys Thr Tyr Glu Met Val Asp Asp Ser Ser Ser Asp Ser Ile
20 25 30

Val Ser Trp Ser Gln Ser Asn Lys Ser Phe Ile Val Trp Asn Pro Pro
35 40 45

Glu Phe Ser Arg Asp Leu Leu Pro Arg Phe Phe Lys His Asn Asn Phe
50 55 60

Ser Ser Phe Ile Arg Gln Leu Asn Thr Tyr Gly Phe Arg Lys Ala Asp
65 70 75 80

Pro Glu Gln Trp Glu Phe Ala Asn Asp Asp Phe Val Arg Gly Gln Pro
85 90 95

His Leu Met Lys Asn Ile His Arg Arg Lys Pro Val His Ser His Ser
100 105 110

Leu Pro Asn Leu Gln Ala Gln Leu Asn Pro Leu Thr Asp Ser Glu Arg
115 120 125

Val Arg Met Asn Asn Gln Ile Glu Arg Leu Thr Lys Glu Lys Glu Gly
130 135 140

Leu Leu Glu Glu Leu His Lys Gln Asp Glu Glu Arg Glu Val Phe Glu
145   150   155   160

Met Gln Val Lys Glu Leu Lys Glu Arg Leu Gln His Met Glu Lys Arg
                165   170   175

Gln Lys Thr Met Val Ser Phe Val Ser Gln Val Leu Glu Lys Pro Gly
            180   185   190

Leu Ala Leu Asn Leu Ser Pro Cys Val Pro Glu Thr Asn Glu Arg Lys
        195   200   205

Arg Arg Phe Pro Arg Ile Glu Phe Phe Pro Asp Glu Pro Met Leu Glu
    210   215   220

Glu Asn Lys Thr Cys Val Val Val Arg Glu Glu Gly Ser Thr Ser Pro
225   230   235   240

Ser Ser His Thr Arg Glu His Gln Val Glu Gln Leu Glu Ser Ser Ile
                245   250   255

Ala Ile Trp Glu Asn Leu Val Ser Asp Ser Cys Glu Ser Met Leu Gln
            260   265   270

Ser Arg Ser Met Met Thr Leu Asp Val Asp Glu Ser Ser Thr Phe Pro
        275   280   285

Glu Ser Pro Pro Leu Ser Cys Ile Gln Leu Ser Val Asp Ser Arg Leu
    290   295   300

Lys Ser Pro Pro Ser Pro Arg Ile Ile Asp Met Asn Cys Glu Pro Asp
305   310   315   320

Gly Ser Lys Glu Gln Asn Thr Val Ala Ala Pro Pro Pro Pro Pro Val
                325   330   335

Ala Gly Ala Asn Asp Gly Phe Trp Gln Gln Phe Phe Ser Glu Asn Pro
            340   345   350

Gly Ser Thr Glu Gln Arg Glu Val Gln Leu Glu Arg Lys Asp Asp Lys
        355   360   365

Asp Lys Ala Gly Val Arg Thr Glu Lys Cys Trp Trp Asn Ser Arg Asn
    370   375   380

Val Asn Ala Ile Thr Glu Gln Leu Gly His Leu Thr Ser Ser Glu Arg
385   390   395   400

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<210> 81
<211> 751
<212> DNA
<213> Arabidopsis thaliana

<220>

<223> G25

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ctcagtgagt gaagaaagag atgggaaacg agagaggaag aatctgtaca gagggataag 240
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atcggaggac ctgatggcat tggaggatta catgagattc tatcagattc cggttgccga 540
cgaccaatcg gcgaccgata ttggaaattt atggagctat caagactcca attaaatctc 600
ttatttcccg gccggtttgc tcactcatta atatgctgct aatttacttg tttttttactt 660
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<212> PRT
<213> Arabidopsis thaliana

<220>
<223> G25

<400> 82
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Ser Glu Pro Ser Gln Leu Gly Ser Val Ser Ser Arg Lys Lys Arg Lys
20 25 30

Pro Val Ser Val Ser Glu Glu Arg Asp Gly Lys Arg Glu Arg Lys Asn
35 40 45

Leu Tyr Arg Gly Ile Arg Gln Arg Pro Trp Gly Lys Trp Ala Ala Glu
50 55 60

Ile Arg Asp Pro Ser Lys Gly Val Arg Val Trp Leu Gly Thr Phe Lys
65 70 75 80

Thr Ala Asp Glu Ala Ala Arg Ala Tyr Asp Val Ala Ala Ile Lys Ile
85 90 95

Arg Gly Arg Lys Ala Lys Leu Asn Phe Pro Asn Thr Gln Val Glu Glu
100 105 110

Glu Ala Asp Thr Lys Pro Gly Gly Asn Gln Asn Glu Leu Ile Ser Glu
115 120 125

Asn Gln Val Glu Ser Leu Ser Glu Asp Leu Met Ala Leu Glu Asp Tyr
130 135 140

Met Arg Phe Tyr Gln Ile Pro Val Ala Asp Asp Gln Ser Ala Thr Asp
145 150 155 160

Ile Gly Asn Leu Trp Ser Tyr Gln Asp Ser Asn
165 170

<210> 83
<211> 2311
<212> DNA
<213> Arabidopsis thaliana

<220>
<223> G610

<400> 83
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tttgattatg taatttggtg gtaggaccat g 2311

<210> 84
<211> 640
<212> PRT
<213> Arabidopsis thaliana

<220>
<223> G610

<400> 84
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Phe Pro Asn Ile Pro Lys Ala Pro Arg Ser Ser Arg Arg Lys Val Ser
            20   25   30

Gly Lys Arg Ser Asp Asp Glu Ser Glu Ile Cys Ala Ile Asp Leu Leu
        35   40   45

Ala Ser Leu Ala Gly Lys Leu Leu Glu Glu Ser Glu Ser Ser Ser Thr
    50   55   60

Ser Thr Tyr Ala Ser Glu Ala Asp Asn Leu Asp His Leu Gly Gly Leu
65   70   75   80

Ile Lys Gln Glu Leu Glu Asp Gly Tyr Thr Thr Lys Pro Cys Lys Ser
                85   90   95

Glu Phe Phe Asp Pro Gly Asn Pro Ala Ser Lys Ser Thr Ser Glu Asn
            100   105   110

Thr Ser Val Thr Cys Leu Pro Phe Ser Ser Phe Glu Asn Asp Cys Ile
        115   120   125

Leu Glu Gln Thr Pro Val Ser Asp Cys Lys Arg Ala Ser Gly Leu Lys
    130   135   140

Ser Leu Val Gly Ser Ile Thr Glu Glu Thr Cys Val Val Asn Glu Asp
145   150   155   160

Ala Gly Ser Glu Gln Gly Ala Asn Thr Phe Ser Leu Lys Asp Pro Ser
                165   170   175

Gln Leu His Ser Gln Ser Pro Glu Ser Val Leu Leu Asp Gly Asp Val
            180   185   190

Lys Leu Ala Pro Cys Thr Asp Gln Val Pro Asn Asp Ser Phe Lys Gly
        195   200   205

Tyr Arg Asn His Ser Lys Leu Val Cys Arg Asp Asp Asp Glu Asn Tyr
    210   215   220

Cys Lys Tyr Tyr Lys Phe Ser Asp Lys Cys Lys Ser Tyr Arg Pro Leu
225   230   235   240

Ser Arg Val Gly Asn Arg Arg Ile Met Gln Ser Val Arg Ala Ile Ser
                245   250   255

Lys Leu Lys Cys Phe Glu Asp Thr Arg Thr Asp Gly Arg Leu Lys Ala
            260   265   270

Leu Tyr Arg Lys Arg Lys Leu Cys Tyr Gly Tyr Asn Pro Trp Lys Arg
        275   280   285

Glu Thr Ile His Arg Lys Arg Arg Leu Ser Asp Lys Gly Leu Val Val
290 295 300

Asn Tyr Asp Gly Gly Leu Ser Ser Glu Ser Val Ser Asn Ser Pro Glu
305 310 315 320

Lys Gly Glu Ser Glu Asn Gly Asp Phe Ser Ala Ala Lys Ile Gly Leu
325 330 335

Leu Ser Lys Asp Ser Arg Val Lys Phe Ser Ile Lys Ser Leu Arg Ile
340 345 350

Pro Glu Leu Val Ile Glu Val Pro Glu Thr Ala Thr Val Gly Leu Leu
355 360 365

Lys Arg Thr Val Lys Glu Ala Val Thr Ala Leu Leu Gly Gly Gly Ile
370 375 380

Arg Ile Gly Val Leu Val Gln Gly Lys Lys Val Arg Asp Asp Asn Asn
385 390 395 400

Thr Leu Ser Gln Thr Gly Leu Ser Cys Arg Glu Asn Leu Gly Asn Leu
405 410 415

Gly Phe Thr Leu Glu Pro Gly Leu Glu Thr Leu Pro Val Pro Leu Cys
420 425 430

Ser Glu Thr Pro Val Leu Ser Leu Pro Thr Asp Ser Thr Lys Leu Ser
435 440 445

Glu Arg Ser Ala Ala Ser Pro Ala Leu Glu Thr Gly Ile Pro Leu Pro
450 455 460

Pro Gln Asp Glu Asp Tyr Leu Ile Asn Leu Gly Asn Ser Val Glu Asn
465 470 475 480

Asn Asp Glu Leu Val Pro His Leu Ser Asp Ile Pro Ala Asp Glu Gln
485 490 495

Pro Ser Ser Asp Ser Arg Ala Leu Val Pro Val Leu Ala Leu Glu Ser
500 505 510

Asp Ala Leu Ala Leu Val Pro Val Asn Glu Lys Pro Lys Arg Thr Glu
515 520 525

Leu Ser Gln Arg Arg Thr Arg Arg Leu Phe Ser Val Thr Glu Val Glu
530 535 540

Ala Leu Val Ser Ala Val Glu Glu Val Gly Thr Gly Arg Trp Arg Asp
545 550 555 560

Val Lys Leu Arg Ser Phe Glu Asn Ala Ser His Arg Thr Tyr Val Asp
565 570 575

Leu Lys Asp Lys Trp Lys Thr Leu Val His Thr Ala Ser Ile Ser Pro
580 585 590

Gln Gln Arg Arg Gly Glu Pro Val Pro Gln Glu Leu Leu Asp Arg Val
595 600 605

Leu Gly Ala His Arg Tyr Trp Thr Gln His Gln Met Lys Gln Asn Gly
610 615 620

Lys His Gln Val Ala Thr Thr Met Val Val Glu Ala Gly Ser Ser Met
625 630 635 640

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<212> DNA
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<223> G229

<400> 85
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20 25 30

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Gly Glu Gly Ser Trp Arg Ser Leu Pro Lys Asn Ala Gly Leu Lys Arg
         35                  40                  45

Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Ser Asp
     50                  55                  60

Leu Lys Arg Gly Asn Ile Thr Pro Glu Glu Glu Glu Leu Val Val Lys
 65                  70                  75                  80

Leu His Ser Thr Leu Gly Asn Arg Trp Ser Leu Ile Ala Gly His Leu
                 85                  90                  95

Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Ser His Leu
            100                 105                 110

Ser Arg Lys Leu His Asn Phe Ile Arg Lys Pro Ser Ile Ser Gln Asp
        115                 120                 125

Val Ser Ala Val Ile Met Ala Asn Ala Ser Ser Ala Pro Pro Pro Pro
    130                 135                 140

Gln Ala Lys Arg Arg Leu Gly Arg Thr Ser Arg Ser Ala Met Lys Pro
145                 150                 155                 160

Lys Ile Arg Arg Thr Lys Thr Arg Lys Thr Lys Lys Thr Ser Ala Pro
                165                 170                 175

Pro Glu Pro Asn Ala Asp Val Ala Gly Ala Asp Lys Glu Ala Leu Met
            180                 185                 190

Val Glu Ser Ser Gly Ala Glu Ala Glu Leu Gly Arg Pro Cys Asp Tyr
        195                 200                 205

Tyr Gly Asp Asp Cys Asn Lys Asn Leu Met Ser Ile Asn Gly Asp Asn
    210                 215                 220

Gly Val Leu Thr Phe Asp Asp Asp Ile Ile Asp Leu Leu Leu Asp Glu
225                 230                 235                 240

Ser Asp Pro Gly His Leu Tyr Thr Asn Thr Thr Cys Gly Gly Gly Gly
                245                 250                 255

Glu Leu His Asn Ile Arg Asp Ser Glu Gly Ala Arg Gly Phe Ser Asp
            260                 265                 270

Thr Trp Asn Gln Gly Asn Leu Asp Cys Leu Leu Gln Ser Cys Pro Ser
        275                 280                 285

Val Glu Ser Phe Leu Asn Tyr Asp His Gln Val Asn Asp Ala Ser Thr
    290                 295                 300

Asp Glu Phe Ile Asp Trp Asp Cys Val Trp Gln Glu Gly Ser Asp Asn
305                 310                 315                 320

Asn Leu Trp His Glu Lys Glu Asn Pro Asp Ser Met Val Ser Trp Leu
                325                 330                 335
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Leu Asp Gly Asp Asp Glu Ala Thr Ile Gly Asn Ser Asn Cys Glu Asn
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Phe Gly Glu Pro Leu Asp His Asp Asp Glu Ser Ala Leu Val Ala Trp
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Leu Leu Ser
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<212> DNA
<213> Arabidopsis thaliana

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<223> G221

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<211> 226
<212> PRT
<213> Arabidopsis thaliana

<220>
<223> G221

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20 25 30

Leu Ile Asn Tyr Ile Ala Asn His Gly Asp Gly Val Trp Asn Ser Leu
35 40 45

Ala Lys Ser Ala Gly Leu Lys Arg Thr Gly Lys Ser Cys Arg Leu Arg
50 55 60

Trp Leu Asn Tyr Leu Arg Pro Asp Val Arg Arg Gly Asn Ile Thr Pro
65 70 75 80

Glu Glu Gln Leu Ile Ile Met Glu Leu His Ala Lys Trp Gly Asn Arg
85 90 95

Trp Ser Lys Ile Ala Lys His Leu Pro Gly Arg Thr Asp Asn Glu Ile
100 105 110

Lys Asn Phe Cys Arg Thr Arg Ile Gln Lys Tyr Ile Lys Gln Ser Asp
115 120 125

Val Thr Thr Thr Ser Ser Val Gly Ser His His Ser Ser Glu Ile Asn
130 135 140

Asp Gln Ala Ala Ser Thr Ser Ser His Asn Val Phe Cys Thr Gln Asp
145 150 155 160

Gln Ala Met Glu Thr Tyr Ser Pro Thr Pro Thr Ser Tyr Gln His Thr
165 170 175

Asn Met Glu Phe Asn Tyr Gly Asn Tyr Ser Ala Ala Ala Val Thr Ala
180 185 190

Thr Val Asp Tyr Pro Val Pro Met Thr Val Asp Asp Gln Thr Gly Glu
195 200 205

Asn Tyr Trp Gly Met Asp Asp Ile Trp Ser Ser Met His Leu Leu Asn
210 215 220

Gly Asn
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<210> 89
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<220>
<223> "n" bases at various positions throughout the
sequence may be A, T, C, G, other or unknown

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<210> 90
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<212> PRT
<213> Arabidopsis thaliana

<220>
<223> G186

<400> 90

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            20                  25                  30

Asn Pro Leu Ala Met Ser Arg Ile Asp Glu Glu Asp Asp Gln Lys Thr
        35                  40                  45

Arg Ile Ser Thr Asn Gly Ser Glu Phe Arg Phe Pro Val Ser Leu Ser
    50                  55                  60

Gly Ile Arg Asp Arg Glu Asp Glu Asp Phe Ser Ser Gly Val Ala Gly
65                  70                  75                  80

Asp Asn Asp Arg Glu Val Pro Gly Glu Val Asp Phe Phe Ser Asp Lys
                85                  90                  95

Lys Ser Arg Val Cys Arg Glu Asp Asp Glu Gly Phe Arg Val Lys Lys
            100                 105                 110
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Glu Glu Gln Asp Asp Arg Thr Asp Val Asn Thr Gly Leu Asn Leu Arg
        115                 120                 125

Thr Thr Gly Asn Thr Lys Ser Asp Glu Ser Met Ile Asp Asp Gly Glu
    130                 135                 140

Ser Ser Glu Met Glu Asp Lys Arg Ala Lys Asn Glu Leu Val Lys Leu
145                 150                 155                 160

Gln Asp Glu Leu Lys Lys Met Thr Met Asp Asn Gln Lys Leu Arg Glu
                165                 170                 175

Leu Leu Thr Gln Val Ser Asn Ser Tyr Thr Ser Leu Gln Met His Leu
            180                 185                 190

Val Ser Leu Met Gln Gln Gln Gln Gln Gln Asn Asn Lys Val Ile Glu
        195                 200                 205

Ala Ala Glu Lys Pro Glu Glu Thr Ile Val Pro Arg Gln Phe Ile Asp
    210                 215                 220

Leu Gly Pro Thr Arg Ala Val Gly Glu Ala Glu Asp Val Ser Asn Ser
225                 230                 235                 240

Ser Ser Glu Asp Arg Thr Arg Ser Gly Gly Ser Ser Ala Ala Glu Arg
                245                 250                 255

Arg Ser Asn Gly Lys Arg Leu Gly Arg Glu Glu Ser Pro Glu Thr Glu
            260                 265                 270

Ser Asn Lys Ile Gln Lys Val Asn Ser Thr Thr Pro Thr Thr Phe Asp
        275                 280                 285

Gln Thr Ala Glu Ala Thr Met Arg Lys Ala Arg Val Ser Val Arg Ala
    290                 295                 300

Arg Ser Glu Ala Pro Met Ile Ser Asp Gly Cys Gln Trp Arg Lys Tyr
305                 310                 315                 320

Gly Gln Lys Met Ala Lys Gly Asn Pro Cys Pro Arg Ala Tyr Tyr Arg
                325                 330                 335

Cys Thr Met Ala Thr Gly Cys Pro Val Arg Lys Gln Val Gln Arg Cys
            340                 345                 350

Ala Glu Asp Arg Ser Ile Leu Ile Thr Thr Tyr Glu Gly Asn His Asn
        355                 360                 365

His Pro Leu Pro Pro Ala Ala Val Ala Met Ala Ser Thr Thr Thr Ala
    370                 375                 380

Ala Ala Asn Met Leu Leu Ser Gly Ser Met Ser Ser His Asp Gly Met
385                 390                 395                 400

Met Asn Pro Thr Asn Leu Leu Ala Arg Ala Val Leu Pro Cys Ser Thr
                405                 410                 415
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Ser Met Ala Thr Ile Ser Ala Ser Ala Pro Phe Pro Thr Val Thr Leu
420 425 430

Asp Leu Thr His Ser Pro Pro Pro Pro Asn Gly Ser Asn Pro Ser Ser
435 440 445

Ser Ala Ala Thr Asn Asn Asn His Asn Ser Leu Met Gln Arg Pro Gln
450 455 460

Gln Gln Gln Gln Gln Met Thr Asn Leu Pro Pro Gly Met Leu Pro His
465 470 475 480

Val Ile Gly Gln Ala Leu Tyr Asn Gln Ser Lys Phe Ser Gly Leu Gln
485 490 495

Phe Ser Gly Gly Ser Pro Ser Thr Ala Ala Phe Ser Gln Ser His Ala
500 505 510

Val Ala Asp Thr Ile Thr Ala Leu Thr Ala Asp Pro Asn Phe Thr Ala
515 520 525

Ala Leu Ala Ala Val Ile Ser Ser Met Ile Asn Gly Thr Asn His His
530 535 540

Asp Gly Glu Gly Asn Asn Lys Asn Gln
545 550

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<212> DNA
<213> Arabidopsis thaliana

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<223> G562

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<212> PRT
<213> Arabidopsis thaliana

<220>
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20 25 30

Trp Ala Ala Met Gln Ala Tyr Tyr Gly Pro Arg Val Ala Met Pro Pro
35 40 45

Tyr Tyr Asn Ser Ala Met Ala Ala Ser Gly His Pro Pro Pro Pro Tyr
50 55 60

Met Trp Asn Pro Gln His Met Met Ser Pro Ser Gly Ala Pro Tyr Ala
65 70 75 80

Ala Val Tyr Pro His Gly Gly Gly Val Tyr Ala His Pro Gly Ile Pro
85 90 95

Met Gly Ser Leu Pro Gln Gly Gln Lys Asp Pro Pro Leu Thr Thr Pro
100 105 110

Gly Thr Leu Leu Ser Ile Asp Thr Pro Thr Lys Ser Thr Gly Asn Thr
115 120 125

Asp Asn Gly Leu Met Lys Lys Leu Lys Glu Phe Asp Gly Leu Ala Met
130 135 140

Ser Leu Gly Asn Gly Asn Pro Glu Asn Gly Ala Asp Glu His Lys Arg
145 150 155 160

Ser Arg Asn Ser Ser Glu Thr Asp Gly Ser Thr Asp Gly Ser Asp Gly
165 170 175

Asn Thr Thr Gly Ala Asp Glu Pro Lys Leu Lys Arg Ser Arg Glu Gly
180 185 190

Thr Pro Thr Lys Asp Gly Lys Gln Leu Val Gln Ala Ser Ser Phe His
195 200 205

Ser Val Ser Pro Ser Ser Gly Asp Thr Gly Val Lys Leu Ile Gln Gly
210 215 220

Ser Gly Ala Ile Leu Ser Pro Gly Val Ser Ala Asn Ser Asn Pro Phe
225 230 235 240

Met Ser Gln Ser Leu Ala Met Val Pro Pro Glu Thr Trp Leu Gln Asn
245 250 255

Glu Arg Glu Leu Lys Arg Glu Arg Arg Lys Gln Ser Asn Arg Glu Ser
260 265 270

Ala Arg Arg Ser Arg Leu Arg Lys Gln Ala Glu Thr Glu Glu Leu Ala
275 280 285

Arg Lys Val Glu Ala Leu Thr Ala Glu Asn Met Ala Leu Arg Ser Glu
290 295 300

Leu Asn Gln Leu Asn Glu Lys Ser Asp Lys Leu Arg Gly Ala Asn Ala
305 310 315 320

Thr Leu Leu Asp Lys Leu Lys Cys Ser Glu Pro Glu Lys Arg Val Pro
325 330 335

Ala Asn Met Leu Ser Arg Val Lys Asn Ser Gly Ala Gly Asp Lys Asn
340 345 350

Lys Asn Gln Gly Asp Asn Asp Ser Asn Ser Thr Ser Lys Phe His Gln
355 360 365

Leu Leu Asp Thr Lys Pro Arg Ala Lys Ala Val Ala Ala Gly
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<212> PRT
<213> Arabidopsis thaliana

<220>
<223> G255

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            20                  25                  30

Gly Glu Gly Cys Trp Arg Ser Leu Pro Arg Ala Ala Gly Leu Leu Arg
        35                  40                  45

Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Asp
    50                  55                  60

Leu Lys Arg Gly Asn Phe Thr His Asp Glu Asp Glu Leu Ile Ile Lys
 65                  70                  75                  80

Leu His Ser Leu Leu Gly Asn Lys Trp Ser Leu Ile Ala Ala Arg Leu
                85                  90                  95

Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr His Ile
            100                 105                 110

Lys Arg Lys Leu Leu Ser Lys Gly Ile Asp Pro Ala Thr His Arg Gly
        115                 120                 125

Ile Asn Glu Ala Lys Ile Ser Asp Leu Lys Lys Thr Lys Asp Gln Ile
    130                 135                 140

Val Lys Asp Val Ser Phe Val Thr Lys Phe Glu Glu Thr Asp Lys Ser
145                 150                 155                 160

Gly Asp Gln Lys Gln Asn Lys Tyr Ile Arg Asn Gly Leu Val Cys Lys
                165                 170                 175

Glu Glu Arg Val Val Val Glu Glu Lys Ile Gly Pro Asp Leu Asn Leu
            180                 185                 190

Glu Leu Arg Ile Ser Pro Pro Trp Gln Asn Gln Arg Glu Ile Ser Thr
        195                 200                 205

Cys Thr Ala Ser Arg Phe Tyr Met Glu Asn Asp Met Glu Cys Ser Ser
    210                 215                 220

Glu Thr Val Lys Cys Gln Thr Glu Asn Ser Ser Ser Ile Ser Tyr Ser
225                 230                 235                 240

Ser Ile Asp Ile Ser Ser Ser Asn Val Gly Tyr Asp Phe Leu Gly Leu
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Lys Thr Arg Ile Leu Asp Phe Arg Ser Leu Glu Met Lys
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<213> Arabidopsis thaliana

<220>
<223> G3

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Gly Ile Arg Arg Arg Lys Trp Gly Lys Trp Val Ala Glu Ile Arg Glu
35 40 45

Pro Asn Lys Arg Ser Arg Leu Trp Leu Gly Ser Tyr Thr Thr Asp Ile
50 55 60

Ala Ala Ala Arg Ala Tyr Asp Val Ala Val Phe Tyr Leu Arg Gly Pro
65 70 75 80

Ser Ala Arg Leu Asn Phe Pro Asp Leu Leu Leu Gln Glu Glu Asp His
85 90 95

Leu Ser Ala Ala Thr Thr Ala Asp Met Pro Ala Ala Leu Ile Arg Glu
100 105 110

Lys Ala Ala Glu Val Gly Ala Arg Val Asp Ala Leu Leu Ala Ser Ala
115 120 125

Ala Pro Ser Met Ala His Ser Thr Pro Pro Val Ile Lys Pro Asp Leu
130 135 140

Asn Gln Ile Pro Glu Ser Gly Asp Ile
145 150

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aagaagaaga tgaagaagag caataaccaa aagaggttta acgaggaaca gatcaagtca 180
cttgagctta tatttgagtc tgagacgagg cttgagccga ggaagaaggt tcaggtagct 240
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<213> Arabidopsis thaliana

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<223> G713

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20 25 30

Arg Phe Asn Glu Glu Gln Ile Lys Ser Leu Glu Leu Ile Phe Glu Ser
35 40 45

Glu Thr Arg Leu Glu Pro Arg Lys Lys Val Gln Val Ala Arg Glu Leu
50 55 60

Gly Leu Gln Pro Arg Gln Met Thr Ile Trp Phe Gln Asn Lys Arg Ala
65 70 75 80

Arg Trp Lys Thr Lys Gln Leu Glu Lys Glu Tyr Asn Thr Leu Arg Ala
85 90 95

Asn Tyr Asn Asn Leu Ala Ser Gln Phe Glu Ile Met Lys Lys Glu Lys
100 105 110

Gln Ser Leu Val Ser Glu Leu Gln Arg Leu Asn Glu Glu Met Gln Arg
115 120 125

Pro Lys Glu Glu Lys His His Glu Cys Cys Gly Asp Gln Gly Leu Ala
130 135 140

Leu Ser Ser Ser Thr Glu Ser His Asn Gly Lys Ser Glu Pro Glu Gly
145 150 155 160

Arg Leu Asp Gln Gly Ser Val Leu Cys Asn Asp Gly Asp Tyr Asn Asn
165 170 175

Asn Ile Lys Thr Glu Tyr Phe Arg Val Gln Gly Glu Thr Asp His Glu
180 185 190

Leu Met Asn Ile Val Glu Lys Ala Asp Asp Ser Cys Leu Thr Ser Ser
195 200 205

Glu Asn Trp Gly Gly Phe Asn Ser Asp Ser Leu Leu Asp Gln Ser Ser
210 215 220

Ser Asn Tyr Pro Asn Trp Trp Glu Phe Trp Ser
225 230 235

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<212> DNA
<213> Arabidopsis thaliana

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ccttttccct tctttttga tcgctgcaga gaaatggaaa ctcctgtggg tttaagattc 180
tgtccgaccg acgaggagat cgtcgtcgat tacctttggc cgaaaaattc cgatagagac 240
acgagccatg tcgatcgatt cattaacaca gtccctgtct gtagactcga tccttgggag 300
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20 25 30

Val Asp Arg Phe Ile Asn Thr Val Pro Val Cys Arg Leu Asp Pro Trp
35 40 45

Glu Leu Pro Cys Gln Ser Arg Ile Lys Leu Lys Asp Val Ala Trp Cys
50 55 60

Phe Phe Arg Pro Lys Glu Asn Lys Tyr Gly Arg Gly Asp Gln Gln Met
65 70 75 80

Arg Lys Thr Lys Ser Gly Phe Trp Lys Ser Thr Gly Arg Pro Lys Pro
85 90 95

Ile Met Arg Asn Arg Gln Gln Ile Gly Glu Lys Lys Ile Leu Met Phe
100 105 110

Tyr Thr Ser Lys Glu Ser Lys Ser Asp Trp Val Ile His Glu Tyr His
115 120 125

Gly Phe Ser His Asn Gln Met Met Met Thr Tyr Thr Leu Cys Lys Val
130 135 140

Met Phe Asn Gly Gly Met Arg Glu Lys Ser Ser Ser Ser Pro Ser Ser
145 150 155 160

Ser Gly Val Ser Gly Ile Glu Gln Ser Arg Arg Asp Ser Leu Ile Pro
165 170 175

Gln Leu Val Asn Asn Ser Glu Gly Ser Ser Leu His Arg Glu Asp Pro
180 185 190

Ser Gln Phe Gly Asp Val Leu Gln Glu Ala Pro Ile Glu Asp Ala Lys
195 200 205

Leu Thr Glu Glu Leu Val Lys Trp Leu Met Asn Asp Glu Asp Asp Ala
    210   215   220

Gln Ile Glu Asp Ala Ile Pro Ile Glu Glu Trp Glu Thr Trp Leu Asn
225   230   235   240

Asp Ile Asp Asp Ala Lys Glu Lys Ser Ile Met Phe Met His Asp Asn
                245   250   255

Arg Ser Asp Tyr Arg Pro Pro Asn Ser Leu Thr Gly Val Phe Ser Asp
            260   265   270

Asp Val Ser Ser Asp Asp Asn Asp Ser Asp Leu Leu Thr Pro Lys Thr
        275   280   285

Asn Ser Ile Gln Thr Ser Ser Thr Cys Asp Ser Phe Gly Ser Ser Asn
    290   295   300

His Arg Ile Asp Gln Ile Lys Asp Leu Gln Glu Ser Pro Thr Ser Thr
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Ile Asn Leu Val Ser Leu Thr Gln Glu Val Ser Ala Ala Ala Asn Asn
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Gln Tyr

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<212> DNA
<213> Arabidopsis thaliana

<220>
<223> G390

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<213> Arabidopsis thaliana

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<223> G390

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Leu Glu Arg Val Tyr Ala Glu Cys Pro Lys Pro Ser Ser Leu Arg Arg
35 40 45

Gln Gln Leu Ile Arg Glu Cys Pro Ile Leu Cys Asn Ile Glu Pro Arg
50 55 60

Gln Ile Lys Val Trp Phe Gln Asn Arg Arg Cys Arg Glu Lys Gln Arg
65 70 75 80

Lys Glu Ser Ala Arg Leu Gln Thr Val Asn Arg Lys Leu Ser Ala Met
85 90 95

Asn Lys Leu Leu Met Glu Glu Asn Asp Arg Leu Gln Lys Gln Val Ser
100 105 110

Asn Leu Val Tyr Glu Asn Gly Phe Met Lys His Arg Ile His Thr Ala
115 120 125

Ser Gly Thr Thr Thr Asp Asn Ser Cys Glu Ser Val Val Val Ser Gly
130 135 140

Gln Gln Arg Gln Gln Gln Asn Pro Thr His Gln His Pro Gln Arg Asp
145 150 155 160

Val Asn Asn Pro Ala Asn Leu Leu Ser Ile Ala Glu Glu Thr Leu Ala
165 170 175

Glu Phe Leu Cys Lys Ala Thr Gly Thr Ala Val Asp Trp Val Gln Met
180 185 190

Ile Gly Met Lys Pro Gly Pro Asp Ser Ile Gly Ile Val Ala Val Ser
195 200 205

Arg Asn Cys Ser Gly Ile Ala Ala Arg Ala Cys Gly Leu Val Ser Leu
210 215 220

Glu Pro Met Lys Val Ala Glu Ile Leu Lys Asp Arg Pro Ser Trp Phe
225 230 235 240

Arg Asp Cys Arg Cys Val Glu Thr Leu Asn Val Ile Pro Thr Gly Asn
245 250 255

Gly Gly Thr Ile Glu Leu Val Asn Thr Gln Ile Tyr Ala Pro Thr Thr
260 265 270

Leu Ala Ala Ala Arg Asp Phe Trp Thr Leu Arg Tyr Ser Thr Ser Leu
275 280 285

Glu Asp Gly Ser Tyr Val Val Cys Glu Arg Ser Leu Thr Ser Ala Thr
290 295 300

Gly Gly Pro Asn Gly Pro Leu Ser Ser Ser Phe Val Arg Ala Lys Met
305 310 315 320

Leu Ser Ser Gly Phe Leu Ile Arg Pro Cys Asp Gly Gly Gly Ser Ile
325 330 335

Ile His Ile Val Asp His Val Asp Leu Asp Val Ser Ser Val Pro Glu
340 345 350

Val Leu Arg Pro Leu Tyr Glu Ser Ser Lys Ile Leu Ala Gln Lys Met
355 360 365

Thr Val Ala Ala Leu Arg His Val Arg Gln Ile Ala Gln Glu Thr Ser
370 375 380

Gly Glu Val Gln Tyr Ser Gly Gly Arg Gln Pro Ala Val Leu Arg Thr
385 390 395 400

Phe Ser Gln Arg Leu Cys Arg Gly Phe Asn Asp Ala Val Asn Gly Phe
405 410 415

Val Asp Asp Gly Trp Ser Pro Met Ser Ser Asp Gly Gly Glu Asp Ile
420 425 430

Thr Ile Met Ile Asn Ser Ser Ser Ala Lys Phe Ala Gly Ser Gln Tyr
435 440 445

Gly Ser Ser Phe Leu Pro Ser Phe Gly Ser Gly Val Leu Cys Ala Lys
450 455 460

Ala Ser Met Leu Leu Gln Asn Val Pro Pro Leu Val Leu Ile Arg Phe
465 470 475 480

Leu Arg Glu His Arg Ala Glu Trp Ala Asp Tyr Gly Val Asp Ala Tyr
485 490 495

Ser Ala Ala Ser Leu Arg Ala Thr Pro Tyr Ala Val Pro Cys Val Arg
500 505 510

Thr Gly Gly Phe Pro Ser Asn Gln Val Ile Leu Pro Leu Ala Gln Thr
515 520 525

Leu Glu His Glu Glu Phe Leu Glu Val Val Arg Leu Gly Gly His Ala
530 535 540

Tyr Ser Pro Glu Asp Met Gly Leu Ser Arg Asp Met Tyr Leu Leu Gln
545 550 555 560

Leu Cys Ser Gly Val Asp Glu Asn Val Val Gly Gly Cys Ala Gln Leu
565 570 575

Val Phe Ala Pro Ile Asp Glu Ser Phe Ala Asp Asp Ala Pro Leu Leu
580 585 590

Pro Ser Gly Phe Arg Val Ile Pro Leu Asp Gln Lys Thr Asn Pro Asn
595 600 605

Asp His Gln Ser Ala Ser Arg Thr Arg Asp Leu Ala Ser Ser Leu Asp
610 615 620

Gly Ser Thr Lys Thr Asp Ser Glu Thr Asn Ser Arg Leu Val Leu Thr
625 630 635 640

Ile Ala Phe Gln Phe Thr Phe Asp Asn His Ser Arg Asp Asn Val Ala
645 650 655

Thr Met Ala Arg Gln Tyr Val Arg Asn Val Val Gly Ser Ile Gln Arg
660 665 670

Val Ala Leu Ala Ile Thr Pro Arg Pro Gly Ser Met Gln Leu Pro Thr
675 680 685

Ser Pro Glu Ala Leu Thr Leu Val Arg Trp Ile Thr Arg Ser Tyr Ser
690 695 700

Ile His Thr Gly Ala Asp Leu Phe Gly Ala Asp Ser Gln Ser Cys Gly
705 710 715 720

Gly Asp Thr Leu Leu Lys Gln Leu Trp Asp His Ser Asp Ala Ile Leu
725 730 735

Cys Cys Ser Leu Lys Thr Asn Ala Ser Pro Val Phe Thr Phe Ala Asn
740 745 750

Gln Ala Gly Leu Asp Met Leu Glu Thr Thr Leu Val Ala Leu Gln Asp
755 760 765

Ile Met Leu Asp Lys Thr Leu Asp Asp Ser Gly Arg Arg Ala Leu Cys
770 775 780

Ser Glu Phe Ala Lys Ile Met Gln Gln Gly Tyr Ala Asn Leu Pro Ala
785 790 795 800

Gly Ile Cys Val Ser Ser Met Gly Arg Pro Val Ser Tyr Glu Gln Ala
805 810 815

Thr Val Trp Lys Val Val Asp Asp Asn Glu Ser Asn His Cys Leu Ala
820 825 830

Phe Thr Leu Val Ser Trp Ser Phe Val
835 840

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<212> DNA
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<223> G1034

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<213> Arabidopsis thaliana

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Leu Phe Asp Asn Asn Leu Asn Pro Val Asp Gly Phe Ser Pro Gln Ser
35 40 45

Phe Asp Arg Asp Tyr Asn Phe Asn Gly Ser Leu Ser Gly Leu Asn Leu
50 55 60

Pro Glu Lys Lys Pro Ile Lys Lys Arg Lys Ser Trp Gly Gln Gln Leu
65 70 75 80

Pro Glu Pro Lys Thr Asn Leu Pro Pro Arg Lys Arg Ala Lys Thr Gln
85 90 95

Asp Glu Lys Glu Gln Arg Arg Val Glu Arg Val Leu Arg Asn Arg Arg
100 105 110

Ala Ala Gln Ser Ser Arg Glu Arg Lys Arg Gln Glu Val Glu Ala Leu
115 120 125

Glu Val Glu Lys Arg Ala Ile Glu Arg Lys Asn Met Asp Leu Glu Met
130 135 140

Arg Leu Ala Asp Met Glu Ala Lys Tyr Tyr Leu Leu Gln Gln Glu Leu
145 150 155 160

Lys Arg Ala Ser Gly Tyr Asn Lys Thr Asn Phe Leu Ser Tyr Ser Asp
165 170 175

Ser Ser Thr Pro Asp Ile Ser Glu Asp Ser Gln Leu Ser Pro Leu Thr
180 185 190

Phe Ser Lys Gln Leu Phe Asn Ala Gln Asp Glu Leu Cys Arg Pro Ile
195 200 205

Ser Pro Gln Ser Ile Gly Pro Leu Thr Ser Arg Thr Val Asp Pro Ser
210 215 220

Thr Leu Ser Pro Lys Ser Leu Ser Ser Pro Asp Ser Ser Asn Ser Asn
225 230 235 240

Ser Ser Asp Met Thr Gln His Pro Ala Val Val Leu Cys Asp Leu Gln
245 250 255

Cys Gln Ser Glu Leu Gly Gln Pro Trp Met Asn Ser Thr Tyr Leu Ser
260 265 270

Leu Arg Thr Lys Ala Leu Lys Leu Ser Val Thr Tyr Leu Ile Thr Met
275 280 285

Leu Thr Thr Phe Leu Ile Val Leu Gly Asn Leu Asn Gln Asn Ile Met
290 295 300

Phe Leu Met Thr Arg Phe Leu Leu Thr Pro Thr Tyr Phe Ile Gln Arg
305 310 315 320

Met Lys Ile Phe Gly Asp Arg Thr Thr Val Phe Ser Met Asn Leu Ser
325 330 335

Tyr Val Ile Phe Ser Thr Met Lys Leu Tyr Gln Thr Arg Val Cys Ile
340 345 350

Arg Ile Ser Leu Leu Gly Arg Arg Gln Ala Cys Ser Arg Asn Leu Ala
355 360 365

Arg Ser Leu Met Asn Ala Thr Met Ala Ala Leu Arg Phe Glu Ser Lys
370 375 380

Gln Arg Leu Phe Arg Asn Phe Leu Ser Thr Val Ala Leu Gln Ile Ser
385 390 395 400

Arg Arg Ser Ser His Phe Leu Trp Tyr
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<212> DNA
<213> Arabidopsis thaliana

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<223> G1149

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<213> Arabidopsis thaliana

<220>
<223> G1149

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            20   25   30

Val Ala Trp Pro Gly Leu Gln Gln Ser Tyr Gly Gly Arg Gly Gly Ser
        35   40   45

Val Ser Ala Gly Arg Gly Arg Gly Asn Val Gly Arg Gly Glu Asn Thr
    50   55   60

Gly Asp Leu Thr Ala Thr Gln Val Pro Val Ala Ser Ala Val Ser Gly
65 70 75 80

Gly Arg Gly Arg Gly Asn Ile Gly Asp Pro Thr Phe Ser Val Ala Ser
85 90 95

Ser Ser Lys Thr Val Ser Val Ala Ser Ser Ser Lys Glu Glu Ser Lys
100 105 110

Asn Thr Glu Val Ser Glu Thr Met Ser Asn Leu Gln Ile Thr Ser Thr
115 120 125

Glu Thr Lys Pro Glu Met Thr Ser Leu Pro Pro Ala Ser Ser Lys Ala
130 135 140

Val Thr Phe Pro Val Arg Pro Gly Arg Gly Thr Leu Gly Lys Lys Val
145 150 155 160

Met Val Arg Ala Asn His Phe Leu Val Gln Val Ala Asp Arg Asp Leu
165 170 175

Tyr His Tyr Asp Val Ser Ile Asn Pro Glu Val Ile Ser Lys Thr Val
180 185 190

Asn Arg Asn Val Met Lys Leu Leu Val Lys Asn Tyr Lys Asp Ser His
195 200 205

Leu Gly Gly Lys Ser Pro Ala Tyr Asp Gly Arg Lys Ser Leu Tyr Thr
210 215 220

Ala Gly Pro Leu Pro Phe Asp Ser Lys Glu Phe Val Val Asn Leu Ala
225 230 235 240

Glu Lys Arg Ala Asp Gly Ser Ser Gly Lys Asp Arg Pro Phe Lys Val
245 250 255

Ala Val Lys Asn Val Thr Ser Thr Asp Leu Tyr Gln Leu Gln Gln Phe
260 265 270

Leu Asp Arg Lys Gln Arg Glu Ala Pro Tyr Asp Thr Ile Gln Val Leu
275 280 285

Asp Val Val Leu Arg Asp Lys Pro Ser Asn Asp Tyr Val Ser Val Gly
290 295 300

Arg Ser Phe Phe His Thr Ser Leu Gly Lys Asp Ala Arg Asp Gly Arg
305 310 315 320

Gly Glu Leu Gly Asp Gly Ile Glu Tyr Trp Arg Gly Tyr Phe Gln Ser
325 330 335

Leu Arg Leu Thr Gln Met Gly Leu Ser Leu Asn Ile Asp Val Ser Ala
340 345 350

Arg Ser Phe Tyr Glu Pro Ile Val Val Thr Asp Phe Ile Ser Lys Phe
355 360 365

Leu Asn Ile Arg Asp Leu Asn Arg Pro Leu Arg Asp Ser Asp Arg Leu
370 375 380

Lys Val Lys Lys Val Leu Arg Thr Leu Lys Val Lys Leu Leu His Trp
385 390 395 400

Asn Gly Thr Lys Ser Ala Lys Ile Ser Gly Ile Ser Ser Leu Pro Ile
405 410 415

Arg Glu Leu Arg Phe Thr Leu Glu Asp Lys Ser Glu Lys Thr Val Val
420 425 430

Gln Tyr Phe Ala Glu Lys Tyr Asn Tyr Arg Val Lys Tyr Gln Ala Leu
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Pro Ala Ile Gln Thr Gly Ser Asp Thr Arg Pro Val Tyr Leu Pro Met
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Glu Leu Cys Gln Ile Asp Glu Gly Gln Arg Tyr Thr Lys Arg Leu Asn
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Glu Lys Gln Val Thr Ala Leu Leu Lys Ala Thr Cys Gln Arg Pro Pro
485 490 495

Asp Arg Glu Asn Ser Ile Lys Asn Leu Val Val Lys Asn Asn Tyr Asn
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Asp Asp Leu Ser Lys Glu Phe Gly Met Ser Val Thr Thr Gln Leu Ala
515 520 525

Ser Ile Glu Ala Arg Val Leu Pro Pro Pro Met Leu Lys Tyr His Asp
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Ser Gly Lys Glu Lys Met Val Asn Pro Arg Leu Gly Gln Trp Asn Met
545 550 555 560

Ile Asp Lys Lys Met Val Asn Gly Ala Lys Val Thr Ser Trp Thr Cys
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Glu Phe Lys Pro Gln Pro Ala Ile Pro Phe Ile Ser Cys Pro Pro Glu
580 585 590

His Ile Glu Glu Ala Leu Leu Asp Ile His Lys Arg Ala Pro Gly Leu
595 600 605

Gln Leu Leu Ile Val Ile Leu Pro Asp Val Thr Gly Ser Tyr Gly Lys
610 615 620

Ile Lys Arg Ile Cys Glu Thr Glu Leu Gly Ile Val Ser Gln Cys Cys
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Gln Pro Arg Gln Val Asn Lys Leu Asn Lys Gln Tyr Met Glu Asn Val
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Ile Met Gly Ala Asp Val Thr His Pro Gln Pro Gly Glu Asp Ser Ser
    690                 695                 700

Pro Ser Ile Ala Ala Val Val Ala Ser Met Asp Trp Pro Glu Ile Asn
705                 710                 715                 720

Lys Tyr Arg Gly Leu Val Ser Ala Gln Ala His Arg Glu Glu Ile Ile
                725                 730                 735

Gln Asp Leu Tyr Lys Leu Val Gln Asp Pro Gln Arg Gly Leu Val His
            740                 745                 750

Ser Gly Leu Ile Arg Glu His Phe Ile Ala Phe Arg Arg Ala Thr Gly
        755                 760                 765

Gln Ile Pro Gln Arg Ile Ile Phe Tyr Arg Asp Gly Val Ser Glu Gly
    770                 775                 780

Gln Phe Ser Gln Val Leu Leu His Glu Met Thr Ala Ile Arg Lys Ala
785                 790                 795                 800

Cys Asn Ser Leu Gln Glu Asn Tyr Val Pro Arg Val Thr Phe Val Ile
                805                 810                 815

Val Gln Lys Arg His His Thr Arg Leu Phe Pro Glu Gln His Gly Asn
            820                 825                 830

Arg Asp Met Thr Asp Lys Ser Gly Asn Ile Gln Pro Gly Thr Val Val
        835                 840                 845

Asp Thr Lys Ile Cys His Pro Asn Glu Phe Asp Phe Tyr Leu Asn Ser
    850                 855                 860

His Ala Gly Ile Gln Gly Thr Ser Arg Pro Ala His Tyr His Val Leu
865                 870                 875                 880

Leu Asp Glu Asn Gly Phe Thr Ala Asp Gln Leu Gln Met Leu Thr Asn
                885                 890                 895

Asn Leu Cys Tyr Thr Tyr Ala Arg Cys Thr Lys Ser Val Ser Ile Val
            900                 905                 910

Pro Pro Ala Tyr Tyr Ala His Leu Ala Ala Phe Arg Ala Arg Tyr Tyr
        915                 920                 925

Met Glu Ser Glu Met Ser Asp Gly Gly Ser Ser Arg Ser Arg Ser Ser
    930                 935                 940

Thr Thr Gly Val Gly Gln Val Ile Ser Gln Leu Pro Ala Ile Lys Asp
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Asn Val Lys Glu Val Met Phe Tyr Cys
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            20                  25                  30

Ser Asp Ser Phe Thr Gly Val Lys Ala Val Thr Thr Glu Ala Glu Gln
        35                  40                  45

Gly Val Val Asp Lys Gln Thr Ser Thr Thr Leu Phe Thr Phe Ser Pro
    50                  55                  60

Gly Gly Glu Lys Ser Ser Arg Asp Val Pro Lys Pro His Val Ala Phe
65                  70                  75                  80
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Ala Met Gln Ser Ala Cys Phe Glu Phe Gly Phe Ala Gln Pro Met Met
                85                  90                  95

Tyr Thr Lys His Pro His Val Glu Gln Tyr Tyr Gly Val Val Ser Ala
            100                 105                 110

Tyr Gly Ser Gln Arg Ser Ser Gly Arg Val Met Ile Pro Leu Lys Met
        115                 120                 125

Glu Thr Glu Glu Asp Gly Thr Ile Tyr Val Asn Ser Lys Gln Tyr His
    130                 135                 140

Gly Ile Ile Arg Arg Arg Gln Ser Arg Ala Lys Ala Glu Lys Leu Ser
145                 150                 155                 160

Arg Cys Arg Lys Pro Tyr Met His His Ser Arg His Leu His Ala Met
                165                 170                 175

Arg Arg Pro Arg Gly Ser Gly Gly Arg Phe Leu Asn Thr Lys Thr Ala
            180                 185                 190

Asp Ala Ala Lys Gln Ser Lys Pro Ser Asn Ser Gln Ser Ser Glu Val
        195                 200                 205

Phe His Pro Glu Asn Glu Thr Ile Asn Ser Ser Arg Glu Ala Asn Glu
    210                 215                 220

Ser Asn Leu Ser Asp Ser Ala Val Thr Ser Met Asp Tyr Phe Leu Ser
225                 230                 235                 240

Ser Ser Ala Tyr Ser Pro Gly Gly Met Val Met Pro Ile Lys Trp Asn
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20 25 30

Lys Ser Ser Gln Val Val Thr Ser Ser Gln Thr Gln Thr Pro Ser Cys
35 40 45

Asp Pro Pro Leu Ile Leu Arg Gly Ser Gly Ser Gly Asp Gly Glu Gly
50 55 60

Asn Gly Pro Leu Pro Gln Pro Pro Pro Pro Leu Tyr His Gln Gln Ser
65 70 75 80

Leu Phe Ile Gln Glu Asp Glu Met Ala Ser Trp Leu His Gln Pro Asn
85 90 95

Arg Gln Asp Tyr Leu Tyr Ser Gln Leu Leu Tyr Ser Gly Val Ala Ser
100 105 110

Thr His Pro Gln Ser Leu Ala Ser Leu Glu Pro Pro Pro Pro Pro Arg
115 120 125

Ala Gln Tyr Ile Leu Ala Ala Asp Arg Pro Thr Gly His Ile Leu Ala
130 135 140

Glu Arg Arg Ala Glu Asn Phe Met Asn Ile Ser Arg Gln Arg Gly Asn
145 150 155 160

Ile Phe Leu Gly Gly Val Glu Ala Val Pro Ser Asn Ser Thr Leu Leu
165 170 175

Ser Ser Ala Thr Glu Ser Ile Pro Ala Thr His Gly Thr Glu Ser Arg
180 185 190

Ala Thr Val Thr Gly Gly Val Ser Arg Thr Phe Ala Val Pro Gly Leu
        195   200   205

Gly Pro Arg Gly Lys Ala Val Ala Ile Glu Thr Ala Gly Thr Gln Ser
    210   215   220

Trp Gly Leu Cys Lys Ala Glu Thr Glu Pro Val Gln Arg Gln Pro Ala
225   230   235   240

Thr Glu Thr Asp Ile Thr Asp Glu Arg Lys Arg Lys Thr Arg Glu Glu
                245   250   255

Thr Asn Val Glu Asn Gln Gly Thr Glu Glu Ala Arg Asp Ser Thr Ser
            260   265   270

Ser Lys Arg Ser Arg Ala Ala Ile Met His Lys Leu Ser Glu Arg Arg
        275   280   285

Arg Arg Gln Lys Ile Asn Glu Met Met Lys Ala Leu Gln Glu Leu Leu
    290   295   300

Pro Arg Cys Thr Lys Thr Asp Arg Ser Ser Met Leu Asp Asp Val Ile
305   310   315   320

Glu Tyr Val Lys Ser Leu Gln Ser Gln Ile Gln Asp Val Leu Asn Gly
                325   330   335

Thr Cys Tyr Asp Ser Thr Asp Asp Val Cys Gly Glu Tyr Thr Thr Thr
            340   345   350

Val His Ala Pro His Gly His Gly Tyr Glu Ser Ala Ser Cys Ile His
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Thr Phe Pro
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<212> PRT
<213> Arabidopsis thaliana

<220>
<223> G241

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Gly His Ser Asn Trp Arg Ala Leu Pro Lys Gln Ala Gly Leu Leu Arg
35 40 45

Cys Gly Lys Ser Cys Arg Leu Arg Trp Met Asn Tyr Leu Lys Pro Asp
50 55 60

Ile Lys Arg Gly Asn Phe Thr Lys Glu Glu Glu Asp Ala Ile Ile Ser
65 70 75 80

Leu His Gln Ile Leu Gly Asn Arg Trp Ser Ala Ile Ala Ala Lys Leu
85 90 95

Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Val Trp His Thr His Leu
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Lys Lys Arg Leu Glu Asp Leu Ser Thr Ser
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ggtggaccaa ctggtcctaa ggtctcttct tctacccttta attactatat tcataacttt 180
gtttgatctt aagataattc atcaagtgtt cttaagttgt ttattttgat ttgtggtggg 240
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tatcatcatc acacg 375

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